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- protein database search, using Smith-Waterman algorithm protein MPsrch_pp

MasPar time 8.60 Seconds 801.905 Million cell updates/sec Thu Oct 22 15:56:22 1998; Run on:

Tabular output not generated.

Title: Description: Perfect Score: Sequence:

..WQKGQREFKRISRSIRKLQC >US-08-848-439-3 (1-275) from US08848439.pep 2073 1 SARGLFLFGQPDFSYKRSNC....

275

PAM 150 Gap 11 Scoring table:

Searched:

69111 segs, 25083644 residues

Post-processing:

summaries 0 8 5 Minimum Match Listing first

Database:

swiss-prot35 1:swiss1

scale 0.642 Variance 72.254; Mean 46.355; Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

tion Pred. No	D PROTEIN PRECU 5.63e-5	RSOR (FR 1.05e-1	3.47e-0	3.8 KD P 1.39e-0	NA POLYM 2.78e-0) IID18 3.99e-0) IID4 (3.99e-0	L PROTEIN S6 K 5.72e-0	TURAL P 8.18e-0	DIATE FILAMENT 1.66e-0	CURONOSYLTRANSF 3.32e-0	ICAL 180.2 KD 6.58e-0	SE SUBUNIT B (1.29e+0	E REGULON TRAN 1.79e+0	LADENOSINE TRAN' 1.29e+0	ATD SYNTHAST 1 296+0		L PROTEIN S6 K 1.79e+0	L PROTEIN S6 K 1.79e+0 ICAL 14.8 KD P 2.48e+0	L PROTEIN S6 K 1.79e+0 ICAL 14.8 KD P 2.48e+0 ICAL 20.1 KD P 2.48e+0	L PROTEIN S6 K 1.79e+0 ICAL 14.8 KD P 2.48e+0 ICAL 20.1 KD P 2.48e+0 YLASE ISOZYME 2.48e+0	L PROTEIN S6 K 1.79e+0 ICAL 14.8 KD P 2.48e+0 ICAL 20.1 KD P 2.48e+0 YLASE ISOZYME 2.48e+0	PROTEIN S6 K 1.79e+ CAL 14.8 KD P 2.48e+ CASE ISOZYME 2.48e+ CASE ISOZYME 2.48e+ CASE ISOZYME 2.48e+
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OI.	RIZ_DRO	ET2_CHIC	T1_CHIC	QI8_CAEE	PC1_GIAL	DI.	PD4_RA	S61_	GO7_BPT	ON3_CA	13_RA	81_YEAS	RB_ACIS	RF_SHI	SGA	ATA_MAIZ	S6A CHIC		BU9_Y	BU9_Y LP2_C	09 X	BU9_Y BU9_Y M2A_C MC2_C	BU9_YEAS LP2_CAEE M2A_ORYS MC2_ORYS
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VACUOLAR ATP SYNTHASE	OMAL PROTEIN S6	PROTEIN	当	HYPOTHETICAL 124.8 KD	COATOMER ALPHA SUBUNIT	PLAKIN I AND I	ITOL 1,4,5-TRISP	4,5-TRIS	SE SUBU	MOVEMENT PROTEIN (CELL	INE DECARBOXYLA	THINE DECARBOXYL	IN, LARGE T-	FORMATE TETRAHYDROFOL	ETICAL PROTEIN	HYPOTHETICAL 71.2 KD P	VACB PROTEIN HOMOLOG.	VACUOLAR PROTEIN SORTI	CYCLASE, AG	FACE P	GER PROTEIN 4
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ALIGNMENTS

	FK12_ P1853	01-NOV-1990 (REL. 16, CREATED)	01-NOV-1990 (REL	FRIZZLED PROTEIN PRECURSOR.	FZ.	DROSOPHILA MELANOGASTER (FRUIT F	EUKARYOTA; METAZOA; ARTH	[1]	SEQUENCE FROM	MEDLINE; 89159415.	. VINSON C.R., CONOVER S., ADLER P.N.; , NATURE 338:263-264(1989).	[2]	SEQUENCE FR	MEDLINE; 91060073.	ADLER P.N., VINS	GENETICS 126:401-416(1990).	-! - FUNCTION: REQUIRED TO COORDINATE THE CYTOSKELETONS OF EPI	CELLS TO PRODUCE A PARALLEL ARRAY OF CUTICULAR HAIRS AND BRIS	FZ IS REQUIRED	TRANSDUCTION.	-! - SUBCELLULAK LOCATION: INTEGRAL MEMBRANE PROTEIN.	-:- ALTERNATIVE PRODUCTS: O-HEDMINAL EBON AA AOS	EMBL: X54648: C804979: -	EMBL: X54649: G804	EMBL: X54650: G804979:	EMBL; X54651; G804979;	EMBL; X54648; G804980;	EMBL; X54649; G804980;	EMBL; X54650; G804980;	EMBL; X5465Z; G8	EMBL; A34040; G/V	EMBL; A34047; G7963; ALI_ DIR. C03540. C03540	PIR: S15708; S1	FLYBASE; FBgn000	TRANSMEMBRANE; SIGNAL;	SIGNAL 1 26 POTENT	CHAIN 27 581	TRANSMEM 248 270	TRANSMEM 281 303	TRANSMEM 336 368	TRANSMEM 381
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DILSGVCFVG -> MYLWQFHTIN (
MISSING (IN CLASS II).
1; 279EBE85 CRC32;
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SEQUENCE FROM N.A.
STRAIN-WHITE LEGHORN; TISSUE-EMBRYONIC BRAIN;
MEDLINE; 94340732.
SERAFINI T., KENNEDY T.E., GALKO M.J., MIRZAYAN C., JES
TESSIER-LAVIGNE M.;
CELL 78:409-424(1994).
-1- FUNCTION: NETRINS CONTROL GUIDANCE OF CNS COMMISSUS
PERIPHERAL MOTOR AXONS.
-1- SUBCELLULAR LOCATION: EXTRACELLULAR.
-1- SIMILARITY: CONTAINS ONE LAMININ N-TERMINAL DOMAIN.
-1- SIMILARITY: CONTAINS ONE C345C DOMAINS.
-1- SIMILARITY: CONTAINS ONE C345C DOMAINS.
-1- SIMILARITY: TO CAENORHABDITIS ELEGANS UNC-6 PROTEIN
EMBL; L34550; G529421; -.
PROSITE; PSO0022; EGF_1; 2.
PROSITE; PSO1248; LAMININ_TYPE_EGF; 3.
GLYCOPROTEIN; EXTRACELLULAR MATRIX; SIGNAL; LAMININ EGIREPEAT.
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LAMININ N-TERMINAL (
3 X LAMININ EGF-LIKE
DOMAIN V-LIKE).
LAMININ EGF-LIKE 1.
LAMININ EGF-LIKE 2.
LAMININ EGF-LIKE 3.
C345C (DOMAIN C).
CELL ATTACHMENT SITE
BY SIMILARITY.
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NETRIN-2.
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NETRIN-1.
LAMININ N-TERMINAL (DOMAIN VI).
3 X LAMININ EGF-LIKE REPEATS (LAMININ
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STRAIN=WHITE LEGHORN; TISSUE=EMBRYONIC BRAIN;
MEDLINE; 94340732.
SERAFINI T., KENNEDY T.E., GALKO M.J., MIRZAYAN C., JE;
TESSIER-LAVIGNE M.;
CELL 78:409-424(1994).
-!- FUNCTION: NETRINS CONTROL GUIDANCE OF CNS COMMISSUI
PERIPHERAL MOTOR AXONS.
-!- SUBCELLULAR LOCATION: EXTRACELLULAR.
-!- SIMILARITY: CONTAINS ONE LAMININ N-TERMINAL DOMAINS.
-!- SIMILARITY: CONTAINS ONE C345C DOMAIN.
-!- SIMILARITY: TO CAENORHABDITIS ELEGANS UNC-6 PROTEIN
EMBL; L34549; G529419; -.
PROSITE; PS00022; EGF_1; 2.
PROSITE; PS01248; LAMININ_TYPE_EGF; 3.
GLYCOPROTEIN; EXTRACELLULAR MATRIX; SIGNAL; LAMININ EGN
REPEAT.
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DOMAIN V-LIKE).
LAMININ EGF-LIKE 2
LAMININ EGF-LIKE 2
LAMININ EGF-LIKE 3
C345C (DOMAIN C).
CELL ATTACHMENT SI
BY SIMILARITY.
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LAST ANNOTATION
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28; M
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01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQU
01-NOV-1997 (REL. 35, LAST ANNC
NETRIN-1 PRECURSOR.
GALLUS GALLUS (CHICKEN).
EUKARYOTA; METAZOA; CHORDATA; V
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KD PROTEIN C45G9.8 IN CHROMOSOME
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1.39e-03;
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STRAIN-BRISTOL N2;
BENTLEY D., WATERSTON R.;
SUBMITTED (FEB-1995) TO EMBL/GENBANK/DDBJ DAEMBL; U21323; G687873; -.
WORMPEP; C45G9.8; CE01859.
HYPOTHETICAL PROTEIN.
DOMAIN 139 145
SEQUENCE 465 AA; 53756 MW; 37C8121B CRC3
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BY SIMILARITY.
BY SIMILARITY.
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RES. 20:1145-1145(1992).
DNA-DEPENDENT RNA POLYMERASE
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Pred. No. 1
19; Mismat
                                                           Score 124;
Pred. No. 3
                                     POTENTIAL
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larity 26.1%;
Conservative
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larity 33.3%;
Conservative
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25; Conser
                                                                  Similarity 31; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-SSP. P1;
MEDLINE; 92195823.
LANZENDOERFER M., 1
NUCLEIC ACIDS RES.
-!- FUNCTION: DNA-1
                                              AA;
                                                                                                                                                                               (REL.
(REL.
(REL.
53.8
 478
493
1118
133
06 2
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YQ18_CAEEL

Q09280;

01-NOV-1995 (R

01-NOV-1995 (R

HYPOTHETICAL 5

C45G9.8.

CAENORHABDITIS

EUKARYOTA; MET
                                                                                                                                                                                                                                                                                                                                                                                                             ESULT 5

D RPC1_GIALA
C P25202;
T 01-MAY-1992 (F
T 01-OCT-1996 (F
E DNA-DIRECTED F
N RPOA3.
S GIARDIA LAMBLI
C EUKARYOTA; PRC
                                                                                                                     KFTVNIIS
DISULFID
DISULFID
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                  Match
                                                            Match
                                                                   Local
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Best Loc
Matches
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                                                                                        456
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                                                                         Matches
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SEQUENCE FROM.

X MEDLINE; 95251650.

A KAWASHIMA H., STROBEL H.W.;

LE BIOCHEM. BIOPHYS. RES. COMMUN. 209:535-540(1995).

C.: - FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE

MONOOXYGENASES. IN LIVER MICROSOMES, THIS ENZYME IS INVOLVED IN AN ADDPH-DEPENDENT ELECTRON TRANSPORT PATHWAY. IT OXIDIZES A VARIETY

C. CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH +

CC CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH +

CC CATALYTIC ACTIVITY: BRAIN.

CC -: SUBCELLULAR LOCATION: MEMBRANE-BOUND.

CC -: SUBCELLULAR BELONGS TO THE CYTOCHROME P450 FAMILY.
                               +
                                                          DIFFERENT
OF RNA POLYMERAS
                                                                                                                                                                                                                                                                                                                                    22
                                                                                                                                                                                                                                                                                                                                                                 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65
                                                                                                     SUBCELLULAR LOCATION: NUCLEAR.
THREE DISTINCT ZINC-CONTAINING RNA POLYMERASES ARE FOUND IN
EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA PRECURSOR,
POLYMERASE II FOR THE MRNA PRECURSOR, AND POLYMERASE III FOR 5S
                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                               PYROPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEMBRANE; HEME;
                                                                                                                                                                                                                                                                                                                                  TICKKSQGFRV-LREMHYEERATKILADVIKHQKDIEKIQELDQR-LRNHVVDPIQALHI
                                                                                                                                                                                                                                                                                                                                                   |:||: :::: ::|: | :| |||: : : | | | : ::| |:: |: ::|:
TLCKNDFALKIKVKEITYINRDTKIILET-KS-KTIYKLNGVSERDLKKSVLWLKDSLQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -DLLKDTLEEESGFLPMLLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRIPHOSPHATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MAMMALIA;
                                                                                                                                                                                                ZINC-FINGER;
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N UPDATE)
(P450 2D-29/2D-3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
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                                                         OF ABOUT 15
T COMPONENT
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                                                                                                                                                                                                                             :-TYPE (POTENTIAL)
DCDCD942 CRC32;
                                                                                                                                                                                               TRANSCRIPTION; ZINC;
RIBONUCLEOSIDE
                             TRIPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HEME (BY SIMILARITY)
F01949B5 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .. 60
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                                                                                                                                                                                                                                                                         DB 1;
2.78e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
99e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FPFS-PNTLLDKAVCNVIASLLFACR-FEYNDPRFIRLL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                         III CONSISTS (IS THE LARGEST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     200
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m
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 100;
Pred. No. 3
22; Mismat
                                                                                                                                                                                                                                                                       Score 101;
Pred. No. 2
25; Mismat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CREATED)
LAST SEQUENCE UPI
LAST ANNOTATION (
(EC 1.14.14.1) (F)
                                                                                                                                                                                                                             2H2-TYP
                              NUCLEOSIDE
 FOUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                        MM;
                                                                                                                                                             AND TRNA GENES.

EMBL; X60325; G9364; -.

DNA-DIRECTED RNA POLYMERASE; T
NUCLEAR PROTEIN.

ZN_FING 79 92 C
SEQUENCE 1741 AA; 193928 MW
 THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (RAT).
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                                                         RNA POLYMERASE
THIS SUBUNIT
                                                                                                                                                                                                                                                                     4.9%;
larity 27.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 26.7%;
16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                446
56683
                               Z
USING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
OF DNA INTO RNA USIN
SUBSTRATES.
CATALYTIC ACTIVITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CPDI_RAT
CPDI_RAT
O64680;
01-NOV-1997 (REL. 35, L
01-NOV-1997 (REL. 35, L
CYTOCHROME P450 IID18 (
CYP2D18 OR CYP2D-18.
RATTUS NORVEGICUS (RAT)
EUKARYOTA; METAZOA; CH(
THTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                            238
                                                                                                                                                                                                                                                                                                                                                                                              237
                                                                                                                                                                                                                                                                                     Similarity 20; Conser
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TCEEMNDINAPYL
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500 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: I
EMBL; U48220; G1:
EMBL; U48219; G1:
PROSITE; PS00086
OXIDOREDUCTASE; I
                                         RNA(N).
SUBUNIT: R
SUBUNITS.
                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 2
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Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173
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MOL. CELL. BIOL. 9:3850-3859(1989).

-!- FUNCTION: PHOSPHORYLATES A WIDE RANGE OF SUBSTRATES INCLUDING
RIBOSOMAL PROTEIN S6.
-!- TISSUE SPECIFICITY: INTESTINE, THYMUS, AND LUNG.
-!- SIMILARITY: THE N-TERMINUS SHOWS HIGH SEQUENCE SIMILARITY TO TH REGIONS OF PROTEIN KINASE C, THE CATALYTIC SUBUNIT OF CAMP-DEPENDENT PROTEIN KINASE, AND CGMP-DEPENDENT PROTEIN KINASE, THE REMINDER OF S6 KINASE II SHOWS HIGH SEQUENCE SIMILARITY TO THE CATALYTIC SUBUNIT OF PHOSPHORYLASE B KINASE.

REMEL; M28489; G556322; -.
RIR; B32571; B32571.
R HSSP; PO5132; ICTP.
R MGD; MGI:104558; RPS6KAI.
R HSSP; PO5132; ICTP.
R MCD: MGI:104558; RPS6KAI.
R PROSITE; PS00110; PROTEIN_KINASE_ATP; 2.
R PROSITE; PS00110; PROTEIN_KINASE_DOM; 2.
R PROSITE; PS50011; PROTEIN_KINASE_DOM; 2.
R TRANSFERASE; SERINE/THREONINE-PROTEIN KINASE; ATP-BINDING; REPEAT; MULTIGENE FAMILY.
R REPEAT; MULTIGENE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEREASFVLHTISKTVEYLHSQGVVHRDLKPSNILYVDESGNPEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       368 MDSICDKVFALIIGEVETLNANPRTSKII-DSADKGIYVLN-407
                                                                                                                                                                                                                                                                 PROTEIN KINASE 1.
PROTEIN KINASE 2.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DS-DNA NONENVELOPED VIRUSES; MYOVIRIDAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        e 99; DB 1;
. No. 5.72e-0
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
PROTEIN GP7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             No. 8.18e
Mismatches
                                                                                                                                                                                                                                                                                                                                     ATP (BY SIMILA ATP (BY SIMILA BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 90384864.

EFIMOV V.P., PRILIPOV A.G., MESYANZHINOV NUCLEIC ACIDS RES. 18:5313-5313(1990).

-!- FUNCTION: STRUCTURAL COMPONENT OF THE EMBL; X15907; G15323; -.

PIR; JQ0657; G7BPT4.

STRUCTURAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98;
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Pred.
13; M
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Pred.
8; M
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LAST SEQI
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larity 39.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 35.2%;
19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                  594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                              664
1 84
1 87
1 87
5 24
5 24
                                                                                                                                                                                                                                                                   310
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90 (REL. 16,
90 (REL. 16,
STRUCTURAL P
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16,
                                                                                                                                                                                                                                               REPEAT; MULTIGENE F
DOMAIN 62
DOMAIN 407
NP_BIND 68
BINDING 94
ACT_SITE 187
NP_BIND 413
BINDING 436
ACT_SITE 524
SEQUENCE 724 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1032 AA;
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nes 16; Conse
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(REL.
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VG07_BPT4
P19061;
01-NOV-1990 (R)
01-NOV-1990 (R)
BASEPLATE STRUG7;
BACTERIOPHAGE 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -LROKFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM STRAIN=D;
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P18520;
01-NOV-1990
01-NOV-1990
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[1]
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est Local
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Matches
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                                                                                                                                                                                                                                                                                                               NAME AND ALTERIAN OF THE ANGUCH I.,

NAME AND HIS MANAGED I., INUGURA C., SUGITA O., KUBOTA I.,

NAME AND H., NOGUCHI T., SASSA S.;

BIOCHEM. BIOPHYS. RES. COMMUN. 156:681-688(1988).

-!- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE

MONOOXYGENASES. IN LIVER MICROSOMES, THIS ENZYME IS INVOLVED IN AN MADPH-DEPENDENT ELECTRON TRANSPORT PATHWAY. IT OXIDIZES A VARIETY

C STRUCTURALLY UNRELATED COMPOUNDS, INCLUDING STEROIDS, FATTY

ACIDS, AND XENOBIOTICS.

-!- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH +

C CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH +

C CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH +

C CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH +

C CATALYTIC ACTIVITY: RH + REDUCED TO HIGH LEVELS IN LIVER AND OTHER

C C CATALYTIC ACTIVITY: REDUCED TO HIGH LEVELS IN LIVER AND OTHER

C C CATALYTIC ACTIVITY: BELONGS TO THE CYTOCHROME P450 FAMILY.

REMBL; X52029; G57816; -.

REMBL; X5203930; -.

REMBL; X5203930; -.

REMBL; X5331; G203830; -.

REMBL; X5331; G203830; -.

REMBL; X5331; G203830; -.

REMBL; X5331; G10873; S16873.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         φ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSPORT; MEMBRANE; HEME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FPFS-PNTLLDKAVCNVIASLLFACR-FEYNDPRFIRLL--DLLKDTLEEESGFLPMLLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SEKII-ALPHA)
                                                                                                                                                               MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S. ₹.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      500;
                                                                                                      (P450-CMF3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JONES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                              TETRAPODA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TETRAPODA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>-</u>.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
:
                       CPD4_RAT
CPD4_RAT
P13108;
01-JAN-1990 (REL. 13, CREATED)
01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
CYTOCHROME P450 IID4 (EC 1.14.14.1) (P450-DB4) (P
(DEBRISOQUINE 4-HYDROXYLASE).
CYP2D14 OR CYP2D-4.
RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPC FUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) DB 1; Le
3.99e-02;
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429F82E7 CRC32;
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ON UPDATE)
A 1 (EC 2.7
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EDUCTASE; MONOOXYGENASE; ELECTRON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 100;
Pred. No. 3
22; Mismat
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, LAST SEQUENCE UPI
, LAST ANNOTATION (
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SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY; TISSUE-LIVE)
MEDLINE; 90189185.
MATSUNAGA E., UMENO M., GONZALEZ F.
T. MOL. EVOL. 30:155-169(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT
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                                                                                                                                                                                                                                                                                             FROM N.A.
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16; Conservative
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56697
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16,
34,
S6 K
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(ARYOTA; METAZOA; C
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89050091.
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P18653;
01-NOV-1990 (REL. 1
01-NOV-1990 (REL. 1
01-OCT-1996 (REL. 1
RIBOSOMAL PROTEIN S
(P90-RSK 1).
RPS6KA1 OR RSK1.
MUS MUSCULUS (MOUSE
EUKARYOTA; METAZOA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA;
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SEQUENCE FROM N.A.
MEDLINE; 89384612.
ALCORTA D.A., CREW
ERIKSON R.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          446
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561_MOUSE
18653;
1-NOV-1990
1-NOV-1990
1-OCT-1996
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MEDLINE;
ISHIDA N.
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EMBL; M2
PIR; D31
PIR; S16
PROSITE;
OXIDORED
MICROSOM
BINDING
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                              GNATHOSTOMATA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          MAMMALIA;
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                                                                                                    INTERMEDIATE
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                                                                                                                                                                 PATTERN;
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IOCHEM. BIOPHYS. RES. COMMUN. 169:260-264(1990).

I- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGAT
SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTIC
ENDOGENOUS COMPOUNDS.

I- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR - UDP +
BETA-D-GLUCORONOSIDE.

I- SUBCELLULAR LOCATION: MICROSOMAL.

I- SUBCELLULAR LOCATION: MICROSOMAL.

I- ALTERNATIVE PRODUCTS: THE UGT1 GENE ENCODES FOR MANY E
UDPGT ISOZYMES WHICH HAVE A DIFFERENT N-TERMINAL DOMAI
COMMON C-TERMINAL DOMAIN OF 245 RESIDUES.
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                                                                                                                      TYPE
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01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
INTERMEDIATE FILAMENT PROTEIN ON3.
CARASSIUS AURATUS (GOLDFISH).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTEICHTHYES; ACTINOPTERYGII; CYPRINIFORMES.
[1]
SEQUENCE FROM N.A.
TISSUE-GLIAL CELL;
MEDLINE; 90180470.
GIORDANO S., GLASGOW E., TESSER P., SCHECHTER N.;
NEURON 2:1507-1516(1989).
-!- FUNCTION: ONE OF THE NONNEURONAL PREDOMINANT INTERPRILAMENT PROTEINS OF THE VISUAL PATHWAY.
-!- SIMILARITY: SIGNIFICANT HOMOLOGY WITH MAMMALIAN TYPE
                                                                                                                                                                                                                                                                                                                                            UD13_RAT STANDARD; PRT; 531 AA.
Q64637;
Q1-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
Q1-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
UDP-GLUCURONOSYLTRANSFERASE 1-3 PRECURSOR, MICROSOMAL (UDPGT) (UGT1*3) (UGT1-03) (UGT1.3) (UGT1-3) (B3).
                                                                                                                                                                                                                                                                   Length
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                                                                                                                                                                  REPEAT
                                                                                                                                                                                                                                                                                    24;
                                                                                                                                                                                                                                                                 e 96; DB 1; L
|. No. 1.66e-01;
| Mismatches 24
                                                                                                                                                                                                                                                CRC32
                                                                                                                                                                  HEPTAD
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COIL 1B.
LINKER 12.
COIL 2.
3E8CCC03
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Pred. No.
14; Misma
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                                                                                                                                                                 COIL;
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-399(1995).
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CHORDATA;
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19; Conservative
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                                                                                                                                    EMBL; M87773; -; NOT_ANN PIR; JS0291; JS0291.
PROSITE; PS00226; IF; 1.
INTERMEDIATE FILAMENT; C DOMAIN 109 420 DOMAIN 421 520 DOMAIN 145. 157 DOMAIN 145. 157 DOMAIN 254 273 DOMAIN 254 273 SEQUENCE 520 AA; 5778
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TISSUE-LIVER;
MEDLINE; 90274676.
SATO H., KOIWAI O.,
BIOCHEM, BIOPHYS. RE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .392
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EUKARYOTA; METAZOA;
EUTHERIA; RODENTIA.
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STRAIN-WISTAR;
MEDLINE; 95332265.
EMI Y., IKUSHIRO S
J. BIOCHEM. 117:393
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                                                                                  TRANSMEMBRANE;
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                                                                                                ALTERNATIVE SPLICING.
POTENTIAL.
UDP-GLUCURONOSYLTRANSFERASE 1
POTENTIAL.
POTENTIAL.
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R; C3B2A846 CRC32;
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Q04781; Q04029;

Q1-NOV-1997 (REL. 35, CREATED)

Q1-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)

Q1-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)

HYPOTHETICAL 180.2 KD PROTEIN IN FAA4-HOR7 INTERGENIC

YMR247C OR YM9408.09C OR YM9920.01C.

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
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BANKS
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A; AEROBIC F
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9-01;
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                                                                                  GLYCOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                 e 94; DB 1; L. No. 3.32e-01; Mismatches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE; 97088999.
YAMAMOTO S., HARAYAMA S.;
INT. J. SYST. BACTERIOL. 46:506-511(1996).
-!- FUNCTION: DNA GYRASE NEGATIVELY SUPERCOILS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MARRELL B.G., RAJANDREAM M TO EMBL/GENBANK/DDBJ DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (FRAGMENTS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
(EC 5.99.1.3) (FRAGMENTS
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6.58e-
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No.
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EMBL/GENBANK,
PROSITE; PS00375; UDPGT; 1.

PROSITE; PS00375; UDPGT; 1.

TRANSFERASE; GLYCOSYLTRANSFERASE; (MULTIGENE FAMILY; MICROSOME; ALTERNSIGNAL 1 25 POTENT 26 531 UDP-GLTRANSMEM 489 505 POTENT CARBOHYD 139 139 POTENT CARBOHYD 293 293 POTENT SEQUENCE 531 AA: 631
                                                                                                                                                                                                                                                                                                                                                  Score
Pred.
15; M
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Pred.
9; M
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Q44273; Q60168;
01-NOV-1997 (REL. 35, CREAT)
01-NOV-1997 (REL. 35, LAST in the control of 
                                                                                                                                                                                                                                                                                                                                                  Similarity 35.7%;
15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 950-1562 FROM
STRAIN=S288C / AB972;
GENTLES S., BOWMAN S., BAI
SUBMITTED (MAR-1995) TO EI
EMBL; Z48639; G732925; -.
EMBL; Z48756; G736313; -.
HYPOTHETICAL PROTEIN.
SEQUENCE 1562 AA; 1801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.4% Similarity 38.8% 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AB972;
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STRAIN-S288C / AB9
HUNT S., BOWMAN S.
SUBMITTED (MAR-199
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                                                             THE
                                 REJOINING
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                                                                                                                                                                                          Gaps
   OCTALYZES THE DOUBLE-STRANDED
                                                    FOR
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                                                                                                                                                                                                                       HYDROLYSIS.
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                                            S RESPONSIBLE ATP HYDROT VOT
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                                                                                                            ANTIBIOTIC RESISTANCE
                                                                                                                                                                                                                                                                                                                                                                                  SONNEI
                                 AND
                                                                                                                                                                                                            LARRLRELSFLNAGVRIVLRDERVALEHIFDLEVGLSEKSAL-DIAGLPGKLA
                                                                                                                                                                       216
                                                                                                                                                                                          Indels
STRANDED DNA IN AN ATP-DEPENDANT MANNER AND ALSO CARINTERCONVERSION OF OTHER TOPOLOGICAL ISOMERS OF DOUD DNA RINGS, INCLUDING CATENANES AND KNOTTED RINGS.

-!- CATALYTIC ACTIVITY: ATP-DEPENDENT BREAKAGE, PASSAGE OF DOUBLE-STRANDED DNA.

-!- SUBUNIT: MADE UP OF TWO CHAINS. THE A CHAIN IS RESPONDENT BREAKAGE AND REJOINING; THE B CHAIN CATALYZES ATP HY ENZYME FORMS AN AZB2 TETRAMER.

EMBL; D73436; G1322131; -.

EMBL; D73421; G1322101; -.

PROSITE; PS00177; TOPOISOMERASE_II; 1.

TOPOISOMERASE; ISOMERASE; ATP-BINDING; ANTIBIOTIC RESISTANTES.
                                                                                                                                                                                                                                                                                                                                                                                                                  [1]
SEQUENCE FROM N.A.
SPECIES=S.DYSENTERIAE; STRAIN=CG097;
YAO R., REDDY L.V., PALCHAUDHURI S.;
SUBMITTED (MAR-1991) TO EMBL/GENBANK/DDBJ DATA BANKS.
[2]
SEQUENCE FROM N.A.
SPECIES=S.FLEXNERI; STRAIN=2A;
MEDLINE; 87032409.
SAKAI T., SASAKAWA C., MAKINO S., YOSHIKAWA M.;
INFECT. IMMUN. 54:395-402(1986).
[3]
SEQUENCE FROM N.A.
SPECIES=S.SONNEI;
MEDLINE; 89212881.
KATO J.I., ITO K.I., NAKAMURA A., WATANABE H.;
INFECT. IMMUN. 57:1391-1398(1989).
                                PASSAGE
                                                                                                                                                                                                                                                                                                                                                                                                    FACULTATIVELY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY TO ARAC FAMILY.

MEDLINE; 92326642.

DORMAN C.J.;

MOL. MICROBIOL. 6:1575-1575(1992).

-!- FUNCTION: TRANSCRIPTIONAL ACTIVATOR OF THE VIRB GEI

ITSELF AN ACTIVATOR OF THE IPAABCD VIRULENCE REGULG.

-!- SIMILARITY: BELONGS TO THE ARAC/XYLS FAMILY OF TRAIRED: X58464; G46954; -.

EMBL; X58464; G46954; -.

EMBL; X16661; G47067; -.

EMBL; X16661; G47067; -.

PIR; S14646; S14646.
                                                                                                                                                                                                                                                                                                                                                                                  SHIGELLA
                                                                                                                                                                       Length
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26;
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29, LAST SEQUENCE UPDATE)
32, LAST ANNOTATION UPDATE)
TRANSCRIPTIONAL ACTIVATOR VIRF
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L.29e+00;
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Pred. No.
23; Misma
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216
23775 MW;
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PLASMID 210 KB INVASION.
PROKARYOTA; GRACILICUTES;
ENTEROBACTERIACEAE.
                                                                                                                                                                                         Conservative
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26
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01-JUN-1994 (REL. 2
01-NOV-1995 (REL. 3
VIRULENCE REGULON 1
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216 7
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004248;

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01-JUN-1994
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SEQUENCE
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30S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ol-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DIMETHYLADENOSINE TRANSFERASE (EC 2.1.1.-) (S-ADENOSYLMETHIONINE-6
N'-ADENOSYL(RRNA) DIMETHYLTRANSFERASE) (16S RRNA DIMETHYLASE) (HIGH
DIMETHYLTRANSFERASE).
KSGA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THE
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N-6-METHYLTRANSFERASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HERRMANN R.;

NUCLEIC ACIDS RES. 24:4420-4449(1996).

-!- FUNCTION: SPECIFICALLY DIMETHYLATES TWO ADJACENT ADENOSINES

LOOP OF A CONSERVED HAIRPIN NEAR THE 3'-END OF 16S RRNA IN 1

LOOP OF A CONSERVED HAIRPIN LEADS TO KASUGAMYCIN RESISTANCE

PARTICLE. ITS INACTIVATION LEADS TO KASUGAMYCIN RESISTANCE

(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104
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SIMILARITY)
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                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                          e 89; DB 1; Len I. No. 1.79e+00; Mismatches 15;
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PROKARYOTA; TENERICUTES; MOLLICUTES; MYCOPLASMA;
MYCOPLASMATACEAE.
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20;
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PROSITE; PS01131; RRNA_A_DIMETH; 1.
MRNA PROCESSING; TRANSFERASE; METHYLTRANSFERASE;
ANTIBIOTIC RESISTANCE.
SEQUENCE 263 AA; 29794 MW; 357AA00D CRC32;
PIR; A60105; A60105.

PROSITE; PS00041; HTH_ARAC_FAMILY_1; 1.

PROSITE; PS01124; HTH_ARAC_FAMILY_2; 1.

PLASMID; VIRULENCE; TRANSCRIPTION REGULATION; 1000 177 196 H-T-H MOTIF (BY SSEQUENCE 262 AA; 30549 MW; 11339B38 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 90; DB 1; Pred. No. 1.29e+00, 11; Mismatches 20
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TO THE RRNA ADENINE
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                                                                                                                                                                                                                            Score 89;
Pred. No.
21; Mism
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                                                                                                                                                                                                                          Similarity 25.5%;
13; Conservative
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20; Conservative
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STRAIN-ATCC 29342 /
MEDLINE; 97105885.
HIMMELREICH R., HIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KSGA_MYCPN STAN P75113; 01-NOV-1997 (REL. 3 01-NOV-1997 (REL. 3 01-NOV-1997 (REL. 3 DIMETHYLADENOSINE T N'-ADENOSYL(RRNA) DELEVEL KASUGAMYCIN RELEVEL KASUGAMYCIN RELE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FAMILY
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Best Local S
Matches 2
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Matches
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algorithm - protein database search, using Smith-Waterman protein MPsrch_pp

MasPar time 9.36 Seconds 509.723 Million cell updates/sec 22 15:54:43 1998; Thu Oct .. 0 Run

not generated

output

Tabular

>US-08-848-439-2 (1-295)_from US08848439 2234 1 MLQGPGSLLLLFLASHCCLG. Title: Description: Perfect Score:

.. WQKGQREFKRISRSIRKLQC Sequence:

295

PAM 150 Gap 11 table: Scoring

seqs, 16180660 residues 131922 Searched

summaries 0 4 5 Match first Minimum Listing Post-processing

Database

a-geneseq32
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28

scale 0.253 Variance 132.088; Mean 33.444; Statistics: No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, derived by analysis of the total score distribution. . 0 2 Pred. N score g and 1s

SUMMARIES

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Result No.	Score	Query Match	Length	DB		escription	Pred. N
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7	g	~	œ		3127	ouse frizzled-8 pro	.35e-2
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		•	9		2661	muscle-specific	.79e+0
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7.34e+00 1.26e+01	.50e+0	.50e+0	.50e+0	.50e+0	.28e+0	.60e+0	.28e+0	.28e+0	.60e+0	.60e+0	.60e+0	.60e+0	.60e+0	.60e+0	.60e+0	.60e+0	.60e+0	.60e+0	.28e+0	.28e+0	.28e+0	.15e+0	.47e+0	.00e+0	.47e+0
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9 7 4																									
19 20																									

ALIGNMENTS

بب ب Gaps ä Length 572; Indels Score 396; DB 27; Pred. No. 2.72e-28; 25; Mismatches 42; Query Match Best Local Similarity 40.7%; Matches 48; Conservative

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-08-848-439-2

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146
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ف
                                                                                                                                                                                                                                           Nusse R, Samos CH, Wangy;

Nusse R, Samos CH, Wangy;

Nusse R, Samos CH, Wangy;

NPPI 97-526631/48.

N-PSDB; T89892.

Identification of Wnt receptor binding modulators - useful for treatment of cancer and growth, development or proliferation related disorders

Disclosure; Page 48-50; 61pp; English.

This protein comprises the mouse transmembrane receptor,

This protein comprises the mouse transmembrane receptor,

This protein comprises the mouse transmembrane receptor,

This protein comprises the mouse and Caenorhabditis elegans

C frizzled-8 (Mfz8), encoded by the Mfz8 gene (see T89892). It is

an example of a Wnt receptor. Other novel frizzled family members

have been identified in human, mouse and Caenorhabditis elegans

(see W31268-74) and are considered also to be Wnt receptors. Wnt

receptors can be used in a novel, claimed method of screening for

compounds which modulate the binding of a Wnt polypeptide (secreted

proteins involved in cell-to-cell signalling) to a Wnt receptor.

Wnt is involved in (mammary) cancer and other processes involving

growth, development and proliferation (both normal and abnormal).

Modulators identified by the claimed method are useful for

treatment of diseases related to these conditions.
103
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                               LDDLDETIQPCHSLCVQVKDRCAPVMSAFGFPWPDMLECDRFP-QDN-DLCIPLASSD
                     slcerardgcealmnkfgfqwperlrcenfpvhgageicvgqntsd
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W31274;
W31274;
Z7-APR-1998 (first entry)
Mouse frizzled-8 protein Mfz8 gene;
Wnt receptor; mouse frizzled-8 protein; Mfz8 gene;
A Wnt receptor; mouse frizzled-8 protein; Mfz8 gene;

a with receptor with transduction; cancer; cell growth; cell prolif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fz5 gene;
cell pro
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5 protein; Hfz5
cell growth; cel
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Mismatches
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W31271;
W31271;
27-APR-1998 (first entry)
Human frizzled-5 protein Mfz5 (Wnt re
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Hsieh J
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US-015307.
V JOHNS HOPKINS.
V LELAND STANFORD J
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US-015307.
JOHNS HOPKINS.
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Local Similarity 43.8%;
nes 56; Conservative
                      -tvldqaippcr
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                                                                                                                                                        Mus musculus.
W09739357-A1.
23-OCT-1997.
11-APR-1997; U
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(STRD ) UNIV I
Andrew D, Bhar
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WO9739357-A1.
23-OCT-1997.
11-APR-1997;
12-APR-1996;
(UYJO ) UNIV
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Best Loc
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Disclosure, Page 37-39; 61pp; English.

This protein comprises the human transmembrane receptor,

frizzled-5 (Hfz5), encoded by the Hfz5 gene (see T89889). It is

an example of a Wnt receptor. Other novel frizzled family members

have been identified in human, mouse and Caenorhabditis elegans

(see W31268-74) and are considered also to be Wnt receptors. Wnt

receptors can be used in a novel, claimed method of screening for

compounds which modulate the binding of a Wnt polypeptide (secreted

proteins involved in cell-to-cell signalling) to a Wnt receptor.

Wnt is involved in (mammary) cancer and other processes involving

growth, development and proliferation (both normal and abnormal).

Modulators identified by the claimed method are useful for

treatment of diseases related to these conditions.
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                                                                                                                  lators - useful for or proliferation related
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This protein comprises the mouse transmembrane receptor,

frizzled-4 (Mfz4), encoded by the Mfz4 gene (see T89888). It is
an example of a Wnt receptor. Other novel frizzled family members
have been identified in human, mouse and Caenorhabditis elegans
(see W31268-74) and are considered also to be Wnt receptors. Wnt
receptors can be used in a novel, claimed method of screening for
compounds which modulate the binding of a Wnt polypeptide (secreted
proteins involved in cell-to-cell signalling) to a Wnt receptor.
Wnt is involved in (mammary) cancer and other processes involving
growth, development and proliferation (both normal and abnormal).

Modulators identified by the claimed method are useful for
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cell proliferation
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Pred. No. 4.69e-26
29; Mismatches 4
                           Nathans
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W09739357-A1.
23-OCT-1997.
11-APR-1997; U06049.
12-APR-1996; US-015307.
(UYJO) UNIV JOHNS HOPKINS.
(STRD) UNIV LELAND STANFORD JUNIOR.
--Arew D, Bhanot P, Brink M, Hsieh J,
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JUNIOR
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27-APR-1998 (first entry)
Mouse frizzled-4 protein Mfz4 (Willian Wit receptor; mouse frizzled-4 pisignal transduction; cancer; celling musculus
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cancer and growth,
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larity 38.8%;
Conservative
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                       Andrew D, Bhanot P,
Nusse R, Samos CH, W
WPI; 97-526631/48.
N-PSDB; T89889.
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                                                                                                                                         cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                              receptors can be used in a novel, claimed method of screening for compounds which modulate the binding of a Wnt polypeptide (secreted proteins involved in cell-to-cell signalling) to a Wnt receptor. Wnt is involved in (mammary) cancer and other processes involving growth, development and proliferation (both normal and abnormal). Modulators identified by the claimed method are useful for treatment of diseases related to these conditions.
                                                     Gaps
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This protein comprises the Caenorhabditis putative transmembrane receptor, frizzled-1, encoded by the Cfz1 gene (see T89887). It is an example of a Wnt receptor. Other novel frizzled family members have been identified in human, mouse and Caenorhabditis elegans (see W31268-74) and are considered also to be Wnt receptors. Wnt receptors can be used in a novel, claimed method of screening for
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                                                                                                                                                                                         TOTABLY:

27-APR-1998 (first entry)

Caenorhabditis frizzled-1 protein Cfz1 (Wnt receptor).

Wnt receptor; Caenorhabditis frizzled-1 protein; Cfz1 gene;

Signal transduction; cancer; cell growth; cell proliferation.

Caenorhabditis elegans.

W09739357-A1.

23-OCT-1997.

11-APR-1997; U06049.

12-APR-1996; US-015307.

(UVJO) UNIV JOHNS HOPKINS.

(UVJO) UNIV JOHNS HOPKINS.

(STRD) UNIV LELAND STANFORD JUNIOR.

Andrew D, Bhanot P, Brink M, Hsieh J, Nathans J,

Nusse R, Samos CH, Wangy;

WPI; 97-526631/48.

N-PSDB; T89887.

Identification of Wnt receptor binding modulators - useful for treatment of cancer and growth, development or proliferation religionsders.

Disclosure; Page 30-31; 61pp; English.
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40;
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57;
    condition
                                 DB 27;
L.51e-25;
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2.46e-24;
                                                     Mismatches
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Pred. No. 2
51; Mismat
                               Score 369;
Pred. No. 1
26; Mismat
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38.3%;
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54; Conservative
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27-APR-1998
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Claim 2; Page 23-25; 61pp; English.

This protein comprises the Drosophila frizzled-2 protein encoded by the Df22 gene (see T89885). It is a receptor for wingless (Wg), acting as a signal transducing molecule, and is an example of a Wnt receptor (WntR). Other novel frizzled family members have been identified in human, mouse and Caenorhabditis elegans (see W31268-74) and are considered also to be Wnt receptors. Wnt receptors can be used in a novel, claimed method of screening for compounds which modulate the binding of a Wnt polypeptide (secreted proteins involved in cell-to-cell signalling) to a Wnt receptor. Wnt is involved in (mammary) cancer and other processes involving growth, development and proliferation (both normal and abnormal). Modulators identified by the claimed method are useful for treatment of diseases related to these conditions.
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er and growth, development or proliferation related
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Drosophila frizzled-2 protein (Wnt receptor) Wnt receptor; Drosophila frizzled-2 protein; wingless receptor; Wg receptor; signal transcell growth; cell proliferation.
Drosophila melanogaster.
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                                                                              ocation/Qualifiers
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US-015307.
7 JOHNS HOPKINS.
7 LELAND STANFORD JANOL P, Brink M, F
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protein Mfz3
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47; Conservative
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W31268;
27-APR-1998 (first e
Mouse frizzled-3 prot
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97-526631/48.
DB; T89885.
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Identification of
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-Q-D-NDLCI
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23-OCT-1997.
11-APR-1997; U12-APR-1996; U
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Similarity
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                                                                                                                                                                                                                                                lators - useful for or proliferation related
                                                                                                                                                                                                                                                                     disorders

I disorders

Disclosure; Page 27-29; 61pp; English.

This protein comprises the mouse frizzled-3 protein encoded by the Mfz3 gene (see T89886), and is a Wnt receptor. Other novel frizzled family members have been identified in human, mouse and Caenorhabditis elegans (see W31268-74) and are considered also to be Wnt receptors. Wnt receptors can be used in a novel, claimed method of screening for compounds which modulate the binding of a wnt polypeptide (secreted proteins involved in cell-to-cell signalling) to a Wnt receptor. Wnt is involved in (mammary) cancer and other processes involving growth, development and proliferation cand other processes involving growth, development and proliferation (both normal and abnormal). Modulators identified by the claimed (both normal and abnormal).
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and proliferation
by the claimed
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                        proliferation.
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   rz3 gene;
cell pro
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Mouse frizzled-6 protein Mfz6 (Wnt receptor).
Wnt receptor; mouse frizzled-6 protein; Mfz6 gene; signal transduction; cancer; cell growth; cell pro
                                                                                                                                                                                                                                                modulators
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.56e-20;
ches 54;
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       Mfz3
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                       growth;
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    frizzled-3 protein;
cancer; cell growt
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Pred.
29; M
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Wnt receptor; mouse frizzled-3 signal transduction; cancer; compus musculus.
W09739357-A1.
23-OCT-1997; U06049.
11-APR-1996; US-015307.
(UYJO) UNIV JOHNS HOPKINS.
(STRD) UNIV LELAND STANFORD JUANGEW D, Bhanot P, Brink M, His Nusse R, Samos CH, Wangy; WPI; 97-526631/48.
N-PSDB; T89886.
Identification of Wnt receptor treatment of cancer and growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; U06049.
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;V JOHNS HOPKINS.
IV LELAND STANFORD J
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larity 33.3%;
Conservative
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Disclosure; Page 41-42; 6
This protein comprises th
frizzled-6 (Mfz6), encode
an example of a Wnt recep
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Mus musculus.

W09739357-A1.
23-OCT-1997.

11-APR-1997; U
12-APR-1996; U
(UYJO) UNIV J
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W31272 stand
W31272;
27-APR-1998
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158
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have been identified in human, mouse and Caenorhabditis elegans (see W31268-74) and are considered also to be Wnt receptors. Wnt receptors can be used in a novel, claimed method of screening for compounds which modulate the binding of a Wnt polypeptide (secreted proteins involved in cell-to-cell signalling) to a Wnt receptor. Wnt is involved in (mammary) cancer and other processes involving growth, development and proliferation (both normal and abnormal). Modulators identified by the claimed method are useful for treatment of diseases related to these conditions.
                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          out-growth modulators derived from EGF-like repeats of netrin 2 - comprise peptide(s) capable of selectively spinal axon out-growth or directing axon orientation ye 48-50; 58pp; English.
                                                                                                                                                                                                                                                                                                        cepitvp-r-cmkmty-nmtffpnlmghydqgiaavemghflhlanlecspniemflcqa
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transgenic animal;
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An ElO chick brain cDNA library was screened with probes base netrin-1 (p78) or netrin-2 (p75) sequences to isolate chick and p75 partial cDNA clones. Full-length clones (given in Q92366-67, respectively) were subsequently obtd. by 3'RACE. is expressed e.g. in COS or insect cells for recombinant p78 prodn., used to breed transgenic animals, or for gene the Sequence 581 AA;
                                                                                                                                                                                                                         709
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Pred. No. 4.86e-17
26; Mismatches 4
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e= "C-terminal
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/label- Domain-VI
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/note= "domain V
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Kennedy T,
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                                                                                                                                                                                                                       Similarity 33.6%;
41; Conservative
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US-152019.
CALIFORNIA.
COLUMBIA NEW
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18-MAY-1995.
08-NOV-1994; U12913.
12-NOV-1993; US-15201
(REGC ) UNIV CALIFORN
(UYCO ) UNIV COLUMBIN
Dodd J, Jessell T,
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Tessier-Lavigne M;
WPI; 95-194086/25.
N-PSDB; 092367.
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Gallus sp.
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R74187 stand:
R74187;
24-DEC-1995
Chick p75.
Neural axon 0
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An El0 chick brain cDNA library was screened with probes based on netrin-1 (p78) or netrin-2 (p75) sequences to isolate chick p78 and p75 partial cDNA clones. Full-length clones (given in Q92366-67, respectively) were subsequently obtd. by 3'RACE. cDNA is expressed e.g. in COS or insect cells for recombinant p78 and p75 prodn., used to breed transgenic animals, or for gene therapy. Sequence 605 AA;
                                                                                                                                                                                                                                                                               protein-
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transgenic animal;
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46;
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4.55e-02;
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R74186 standard; Protein; 605 AA.
R74186;
24-DEC-1995 (first entry)
Chick p78.
Neural axon out-growth modulator; epidermal gronetrin-1; p78; neurodegenerative disease; transgene therapy.
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Pred. No. 4
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1993; US-152019.
UNIV CALIFORNIA.
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Jessell T, Kennedy T,
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larity 26.1%;
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Tessier-Lavigne M;
WPI; 95-194086/25.
N-PSDB; Q92366.
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12-NOV-1993;
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This protein comprises human netrin-1 (see W35946), a protein which is involved in neural axon guidance, and which is especially useful in modulating neural axon outgrowth. Its amino acid sequence was deduced from a cDNA clone (see T97129) isolated from a human foetal brain cDNA library. Neuron growth, differentiation or morphology can be altered by contact with netrin (claimed). Isolated netrin-1 can also be used to screen chemical libraries for candidate drugs suitable for diagnosis or treatment of diseases associated with undesirable neural cell growth, by comparing binding to a netrin binding target with and without the presence of a prospective agent. Agents that modulate the interaction may be
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Is for d
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screening; human
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                                                                                                                                                                                                                                                                                     Human netrin-1 protein and related nucleic acids - us modulating neuron growth and screening for compounds or treatment of diseases associated with undesirable Claim 1; Page 13-15; 22pp; English.
This protein comprises human netrin-1 (see W35946), a which is involved in neural axon guidance, and which
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Pred. No. 8.16e-02
30; Mismatches 4
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useful as pharmaceutical lead
Sequence 604 AA;
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9-APR-1996; US-635137.
EXEL-) EXELIXIS PHARM INC.
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diagnosis;
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29; Conservative
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Human netrin-1.
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WPI; 97-535773/49.
N-PSDB; T97129.
                                                                                Netrin-1; neuron;
               standard;
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WO9740064-A1
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R74188 stand
R74188;
24-DEC-1995
Mouse P78.
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06-DEC-1996; U
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Claim 7; Page 42-44; 53pp; English.

Claim 7; Page 42-44; 53pp; English.

This protein sequence comprises the human RECK protein (reversion-inducing cysteine rich protein with Kazal motif), which is capable of transforming malignant cancer cells with an activated ras gene into normal cells (reversion activity). Its amino acid sequence into normal cells (reversion activity). Its amino acid sequence was deduced from a cDNA clone (see T90508) obtained from human fibroblast MRC-5 (ATCC CCL 171) cells. A claimed method for treatment of cancer comprises contacting the cancer cells with a RECK polypeptide. RECK may also be expressed using gene therapy methods for in vivo treatment of cancer.
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                                                                                                                                                                                                                      Neural axon out-growth modulators derived from EGF-like repeats netrin 1 or netrin 2 - comprise peptide(s) capable of selective increasing spinal axon out-growth or directing axon orientation Claim 1; Page 51-52; 58pp; English.

Chick p75 and p78 sequences (given in R74186-87, respectively) were used to identify conserved amino acid regions, which were then used to design degenerate primers for the amplification of a fragment of the mouse p78 cDNA (Q92368). This cDNA can be expressed in host cells for recombinant p78 prodn, or used to breed transgenic animals, or for gene therapy.
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RECK cancer-inhibiting protein.
reversion-inducing cysteine rich protein with Kazal
reversion-therapy; diagnosis.
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Pred. No. 1.70e+
25; Mismatches
                                                                                                                                              Σ
                                                                                                                                              Placzek
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396..415
/label= Kazal_domai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             corresponding protein
(REGC ) UNIV CALIFORNIA.
(UYCO ) UNIV COLUMBIA NEW YORK.
Dodd J, Jessell T, Kennedy T,
Tessier-Lavigne M;
WPI; 95-194086/25.
N-PSDB; Q92368.
netrir
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Local Similarity 23.5%;
les 24; Conservative
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10-JUL-1997.
24-DEC-1996; U20812.
27-DEC-1995; JP-340469.
(AMGE-) AMGEN INC.
(KITA/) KITAYAMA H.
(NODA/) NODA M.
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LID.
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SANKYO CO
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W26642 standa
W26642;

DT 11-FEB-1998

DE Human RECK ca
KW human; cancer
OS HOMO sapiens.
FH Key

FT Domain

FT Domain

FT W09724439-A1.

PR 27-DEC-1996;

PR 27-DEC-1996;

PR 27-DEC-1996;

PR 27-DEC-1996;

PR (KITA/) KITAY

RODA/) NODA

RAMGE-) AMGEN

RAMGEN

RAMGEN
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Homo sapiens
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Length

25;

DB

100;

Score

596 .

Query Match

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ANSTR ) ASTRA AB.

ALS CALLIDYDO, US-130029.

ALS ARRA AB.

ALM RA, Smith D;

ALM RA, Smith D;

NP-15012/46.

NP-1
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activator;
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                                                                                                                   diagnosis.
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                               Indels
                                                                                                                                                                                                                                                                                                                                           W55368 standard; Protein; 804 AA.
W55368;
17-JUN-1998 (first entry)
H. pylori ORF 09ap11406orf2 protein.
Cytoplasmic; vaccine; prevention; treatment; infection; identification; binding compound; bacteria; life cycle; inhibitor; duodenal ulcer disease; chronic gastritis; di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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19;
No. 4.26e+00;
Mismatches 36;
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I. No. 5.11e+00;
Mismatches 19
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Pred. No.
16; Misma
  Pred.
15; N
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kinase (MuSK)
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DMLECDRFPQDNDL--CIPLAS
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 Similarity 30.5%, 25; Conservative
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US-761318.
US-625811.
US-758731.
US-736905.
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DMLECDRFPQDNDL-
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Sest Local Similarity
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muscle-specific
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W26610;
Z7-JAN-1998
Rat musc1
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encoding human agrin and muscle specific kinase - used in diagnosis and treatment of disorder
 rat;
 specific kinase; MuSK; Dmk;
                                                                                                                                                                                                                     Length 868;
                                                                                                                                                                                                                    Score 96; DB 25; Le
Pred. No. 8.79e+00;
12; Mismatches 28;
                                    _domain
                                               Transmembrane_domain
                                                         Intracellular_domain
                                     Extracellular
               Location/Qualifiers 1..19
                           Sig_peptide
      therapy
Receptor tyrosine kinase; muscle
ligand; agrin; diagnosis; therapy
Rattus sp.
                                                                                                                                                                                                                    Query Match
Best Local Similarity 29.7%;
Matches 19; Conservative
                         /label = S
21..492
/label = E
493..521
/label = T
522..868
/label = I
                     Peptide
                                Domain
                                          Domain
                                                     Domain
                Key
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22 15:56:03 1998 Thu Oct secs. Search completed: Job time : 80 secs

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lfca

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R-CA 126

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Gaps

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VAAYYTNYTNGGNCAYG 199 saaccttctgggccaca 322 ..

gctggtgaaggtgcagt NY TNGTNA TGAARCART 439 Ÿ NGTNTGYYTNGAYGAYY cgtgtgcaccg-tg-

gegecagggetgegaag

NAARGAYMGNTGYGCNC ctgcgagcacttcccgc

439

16-JUL-1993 ô ಲ್ಲ

(frizzled) homologue

) osteogarcoma cDNA to

athi; Myomorpha; Muridae; Chordata; tazoa;

Strewler, G.J. and ooks, M., Bradley, M.S., , C.D.,

gene frizzled (fz)

are

Dec 9 09:05

9-2-transinge % % %

SEDGTPALLTTAPP SGLQPGAGGTPGGPGGGAPPRYATLEHPFHCPRVLKVPSYLSY KFLGERDCAAPGEPARPDGSMFFSHHHTRFARLWILTWSVLCCASTFFTVTTSLVAMQ RFRYPERPIIFLSGCYTMVSVAYIAGFVLQERVVCNERFSEDGYRTVGQGTKKEGCTI LFMMLYFFSMASSIWWVILSLTWFLAAGMKWGHAAIEANSQYFHLAAWAVPAVKTITI LAMSQIDGDLLSGVCFVGLNRLDPLRGFVLAPLFVYLFIGTSFLLAGFVSLFRIRTIM KHDGTKTEPLERLMVNISVESVLYTVPATIVIACYFYEQAFREHWERSWVSQHCKSLA KYLMILIVGITSGFWIWSGKTLHSWRKFYTRLTNSRHG OPISIPLCTDIAYNOTIMPNLLGHTNQEDAGLEVHQFYPLVKVQCSPELRFFLCSMYA PVCTVLEQAIPPCRSICERARQGCEALMNKFGFQWPERLRCEHFPRHGAEQICVGQNH /db_xref="PID:g310115" /translation="MRARSALPRSALPRLLLPLLLPAAGPAQFHGEKGISIPDHGFC **IPCPAHYTPRTSPDFTVYMI**

д **266** 662 c ETTV" 299 BASE COUNT

Gaps 3 Length 1912; Indels Mismatches 138; 2.64e-06; DB 90; Score 52; Pred. No. 41; 7,1%; Conservative Best Local Similarity 118; Query Match Matches

2;

140 TNCARYTNIGYCAYGGNATNGARTAYCARAYAIGMGNYTNCCNAAYYTNYTNGGNCAYG 224 tecegetytygacategeetacaaceagaceateatgeecaacettettygygeaca :: -:: -5 Š

343 284 cgaaccaagaggacgcgggcctggaggtgcatcaattctacccgctggtgaaggtgcagt g

200 ARACNATGAARGARGTNYTNGARCARGCNGGNGCNTGGATNCCNYTNGTNATGAARCART

400 gctcgcccgagctgcgcttcttcctgtgctccatgtacgctccggtgtgcacgg-tg--c 344 පු δ

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460 tctgcgaacgcgcgccaaggctgcgagg 260 GYCAYCCNGAYACNAARAARTTYYTNTGYWSNYTNTTYGCNCCNGTNTGYYTNGAYGAYY ð

319

379 TNTGYGTNCARGTNAARGAYMGNTGYGCNC Š ccgagcgcctccgctgcgagcatttcccgc CNGAYATGYTNGARTGYGAYMGNTTYCCNC 461 cgctcatgaacaagttcggcttccagtggc | | |||: | ||||| ||||| 380 CNGTNATGWSNGCNTTYGGNTTYCCN1GJC 임

standard; DNA; INV; 3457 RESULT

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6 BP

CET23D8 281128;

e1008304

Version 5) 21-0CT-1996 (Rel. 49, Created) 01-MAR-1997 (Rel. 51, Last updated,

Caenorhabditis elegans cosmid T23D8 CD63 antigen like; Drosophila tissue polarity protein like; histone H2A; histone H4; Mouse bright protein like;

Rhabditina; Rhabditoidea;

Eukaryotae; mitochondrial eukaryotes; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabdito Rhabditidae; Peloderinae; Caenorhabditis.

Caenorhabditis elegans transporter protein.

1-34576

Wild A.;

Submitted (21-OCT-1996) to the EMBL/GenBank/DDBJ databases

Nematode Sequencing Project, Sanger Centre, Hinxton, Cambridge CB10 1RQ, England and Department of Genetics, Washington University, St. Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or

rw@nematode.wustl.edu

, (frizzled) homologue"

****	(TM)
*****	'

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*******)

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

MasPar time 9.06 Seconds 817.121 Million cell updates/sec Run on:

Thu Oct 22 15:50:45 1998;

not generated. Tabular output

Title: Description: Perfect Score: Sequence:

....WQKGQREFKRISRSIRKLQC >US-08-848-439-2 (1-295) from US08848439.pep 2234 1 MLQGPGSLLLLFLASHCCLG....

295

Scoring table:

PAM 150 Gap 11

69111 seqs, 25083644 residues Searched:

summaries Post-processing: Minimum Match 0% Listing first 45

swiss-prot35
1:swiss1 Database:

scale 0.653 Variance 71.562; Mean 46.742; Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		ď					
Result No.	Score	Query	Length	DB		ription	Pred. No.
l I	33	•	တ်		FRIZ_DROME	RIZZLED PROTEIN PREC	.66e-5
7	マ	•	$\boldsymbol{\omega}$		T2_CHIC	ETRIN-2 PRECURSOR	.14e-1
m	124	5.6	909	Н	NET1_CHICK	ETRIN-1 PRECURSOR.	90
4	0	•	9	Н	OI8_CAEE	POTHETICAL 53.8	.32e-0
ហ	0	•	0		D4_RA	HROME P450 I	.13e-0
Q	0	٠	0	Н	PDI_R	YTOCHROME P450 IID18	.13e-0
7	0	4.5	4	Н	PC1_GIAL	NA-DIRECTED RNA POLY	.73e-0
8	6 6	•	2	⊣	S61_MOU	OSOMAL PROTEIN	.67e-0
თ	86	4.4	ന	-	307_B	ASEPLATE STRUCTURAL	.13e-0
	96	4.3	7	٦	ON3_CAF	NTERMEDIATE FILAMENT	.66e-0
러	94	4.2	ന	-	۳	DP-GLUCURONOSYLTRA	.35e-0
	92	4.1	9	Н	M81_YEAS	OTHETICAL 180.	.68e-0
	06	٠	⊣	Н	RB_A	GYRASE SUBUNI	.31e+0
	89	٠	9	⊣	RF_SHID	IRULENCE REGULON TRA	.83e+0
	06	٠	φ	⊣	3A_MYCP	METHYLADENOSINE	.31e+0
	06	٠	Ø	-	TA_MAIZ	ACUOLAR ATP S	.31e+0
	6 8	•	വ	-1	6A_CHIC	EIN	.83e+0
	88	٠	2	-	U9_YEAS	OTHETICAL 14.8 K	.55e+0
	88	•	$\boldsymbol{\omega}$	~	P2_C	OTHETICAL 20.1 KD	.55e+0
	88	•	4	Н	2A_ORYS	-AMYLASE I	55e+0
	88	•	4	⊣	2_ORYS	ALPHA-AMYLASE ISOZYME	.55e+0
	87	ي 9.	4		YHE2_PSEAE	CAL 50.0	.53e+0
	87	•	⊣	러	- 4	ONCONEURAL VENTRAL ANT	.53e+0

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0	.55e+0	.55e+0	.55e+0	.55e+0	.53e+0	.53e+0	.53e+0	.53e+0	.53e+0	4.88e+00	.88e+0	.88e+0	.72e+0	.88e+0	.88e+0	.88e+0	.72e+0	.72e+0	.72e+0	.72e+0	6.72e+00
ACUOLAR ATP SYNTHA	RIBOSOMAL PROTEIN S6 K	ROTEIN S6	Ы	HYPOTHETICAL 124.8 KD	COATOMER ALPHA SUBUNIT	DESMOPLAKIN I AND II (FIBRONECTIN PRECURSOR	ITOL 1,4,5-TR	1,4	EIN (CE	NE DECARBO	NE DECARBOXYL	IN, LARGE T	FORMATE TETRAHYDROFOL	HYPOTHETICAL PROTEIN M	VACB PROTEIN HOMOLOG.	OTEIN SOR	ITE SURFACE PR	SURFACE P	TE SURFACE PR	ZINC FINGER PROTEIN 40
ATA_	KS62_MOUSE	Θ	NFM_MOUSE	YK64_CAEEL	COPA_YEAST	DESP_HUMAN	×	ايم	IP3R_RAT	VMP_CAMVD	œ	ဥ	E1BL_ADE02	HS_	70_METJ	m'	16_YEAS	MSP1_PLAFF	r.	MSP1_PLAFP	Σ.
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87	8 8 8	88	88	88	87	87	87	87	87	86	86	86	82	86	86	86	82	8 2	8 2	82	82
24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	3 3	40	41	42	43	44	45

ALIGNMENTS

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NEOGNATHAE;
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                                           Gaps
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               (II
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                                                                                                                                                                                                                                                          (LAMININ
                                                                                                                                                                                              (DOMAIN VI)
                                                                      SLYVPVC-TILERPIPPCRSLCESARV-CEKLMKTYNFNWPENLECSKFPVHGGEDLCVA
                                                    -T-ISICKNIPYNMTIMPNLIGHTKQEEAGLEVHQFAPLVKIGCSDDLQLFLC
                                                         CLASS
                                                                                                                                                                               AXONS
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9
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3 X LAMININ EGF-LIKE REPEATS (
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                                           Indels
POTENTIAL.
POTENTIAL.
POTENTIAL.
DILSGVCFVG -> MYLWQFHTIN (
MISSING (IN CLASS II).
V; 279EBE85 CRC32;
                                 Length
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                                      3;
47;
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                                      m
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DOMAIN V-LIKE).
LAMININ EGF-LIKE
LAMININ EGF-LIKE
LAMININ EGF-LIKE
C345C (DOMAIN C).
                                 DB 1;
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BY SIMILARITY.
                                      No. 9.66e
Mismatches
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NETRIN-2.
                                 332;
                                Score
Pred. |
22; M
                        XX.
                                  •• ••
                                 14.98
37.58
                       ~
                                     Similarity 37.5% 45; Conservative
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439
492
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415
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15
581
261
430
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472
530
406
416
81
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TRANSMEM
TRANSMEM
TRANSMEM
VARSPLIC
VARSPLIC
SEQUENCE
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                                 Query Match
                                     Local
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CHAIN
DOMAIN
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DOMAIN
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (LAMININ
                                                                                                                                                                                                                     IPAINPTSLVTSTE-APADCDSYCKPAKGNYKINMKKYCKKDYVVQVNILEMETVANWAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AXONS
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3 X LAMININ EGF-LIKE REPEATS (DOMAIN V-LIKE).
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090922;
01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
01-NOTION N.A.
01-NOTION N.A.
01-NOTION NETRINS CONTROL GUIDANCE OF CNS COMMISSUE
01-NOTION: NETRINS ONE LAMININ EGF-LIKE DOMAIN
01-NOTICAL TYPE CONTAINS ONE C345C DOMAIN
01-NOTICAL TYPE CABNORHABDITIS ELEGANS UNC-6 PROTEIN
01-NOV-19997 (RELLULAR TYPE CABNORHABDITIS SIGNAL; LAMININ EGF
01-NOV-19997 (RELLULAR TYPE CABNORHABDITIS SIGNAL; LAMININ EGF
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LAMININ EGF-LIKE 1
LAMININ EGF-LIKE 2
LAMININ EGF-LIKE 3
LAMININ EGF-LIKE 3
C345C (DOMAIN C).
CELL ATTACHMENT S)
BY SIMILARITY.
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32, LAST SEQUENCE UPDATE)
32, LAST ANNOTATION UPDATE)
KD PROTEIN C45G9.8 IN CHROMOSOME
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P13108;
01-JAN-1990 (REL. 13, CREATED)
01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
CYTOCHROME P450 IID4 (EC 1.14.14.1) (P450-DB4) (F
(DEBRISOQUINE 4-HYDROXYLASE).
CYP2D14 OR CYP2D-4.
RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPC
                                                                                                                                                                                                    41;
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No. 1.32e-03
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01-NOV-1995 (REL. 32, CALITICAL ST. LAST SEQUENCE CL. 101-NOV-1995 (REL. 32, LAST SEQUENCE CL. 101-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
HYPOTHETICAL 53.8 KD PROTEIN C45G9.8 IN CHROMC C45G9.8.

CAENORHABDITIS ELEGANS.
CAENORHABDITIS CAENORHAMATES, NEMATERSTON.
CASCOLE 1095, DAI.
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larity 33.3%;
Conservative
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STRAIN-SPRAGUE-DAWLEY; T
MEDLINE; 90189185.
MATSUNAGA E., UMENO M.,
J. MOL. EVOL. 30:155-169
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P SEQUENCE OF 177-500 F.C.

X MEDLINE; 89050091.

XA ISHIDA N., TAWARACI Y., INUZUKA C., SUGIIA C.

RL SASZATO H., NOGUCHI T., SASSA S.;

RL NAKAZATO H., NOGUCHI T., SASSA S.;

RL BIOCHEM. BIOPHYS. RES. COMMUN 156:681-688(1988)

CC -1- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE

CC MONOOXYGENASES. IN LIVER MICROSOMES, THIS ENZYME IS INVOLVED IN AN NADPH-DEPENDENT ELECTRON TRANSPORT PATHWAY. IT OXIDIZES A VARIETY

CC ACIDS, AND XENOBIOTICS.

CC -1- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH +

CC COXIDIZED FLAVOPROTEIN + H(2) O.

CC -1- INDUCTION: P450 CAN BE INDUCED TO HIGH LEVELS IN LIVER AND OTHER

TISSUES BY VARIOUS FOREIGN COMPOUNDS, INCLUDING DRUGS, PESTICIDES,

AND CARCINOGENS.

CC -1- SUBJECTION: BELONGS TO THE CYTOCHROME P450 FAMILY.

CS -1- RILLARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 95251650.

KAWASHIMA H., STROBEL H.W.;

KAWASHIMA H., STROBEL H.W.;

BIOCHEM. BIOPHYS. RES. COMMUN. 209:535-540(1995).

L. FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE

MONOOXYGENASES. IN LIVER MICROSOMES, THIS ENZYME IS INVOLVED IN AN

C STRUCTURALLY UNRELATED COMPOUNDS, INCLUDING STEROIDS, FATTY

OF STRUCTURALLY UNRELATED COMPOUNDS, INCLUDING STEROIDS, FATTY

ACIDS, AND XENOBIOTICS.

-!- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH +

OXIDIZED FLAVOPROTEIN + H(2)O.

C -!- SUBCELLULAR LOCATION: MEMBRANE-BOUND.

C -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.

EMBL: U48219; G1200518; -.

EMBL: U48219; G1200516; -.

PROSITE; PS00086; CYTOCHROME_P450; 1.

W OXIDOREDUCTASE; MONOOXYGENASE; ELECTRON TRANSPORT; MEMBRANE; HEME;

MICROSOME.

T BINDING 446 HEME (BY SIMILARITY).
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LAST SEQUENCE UPDATE)
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6.13e-03;
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Pred.
28; M
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18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              446
56697
                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: BELONGS TEMBL; X52029; G57816; -.
EMBL; M22331; G203830; -.
PIR; D31579; D31579.
PIR; S16873; S16873.
PROSITE; PS00086; CYTOCHROXIDOREDUCTASE; MONOOXYGEMICROSOME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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O64680;
O1-NOV-1997 (REL. 35, C.
O1-NOV-1997 (REL. 35, L.
O1-NOV-1997 (REL. 35, L.
CYTOCHROME P450 IID18 (
CYP2D18 OR CYP2D-18.
RATTUS NORVEGICUS (RAT)
EUKARYOTA; METAZOA; CHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (RAT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | | | : :: : | ::::
LEQAGAWIPLVMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA;
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SEQUENCE
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RAT
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MUS MUSCULUS (MOUSE)
EUKARYOTA; METAZOA;
EUTHERIA; RODENTIA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T4
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VIRIDAE; DS-DNA
[1]
                                                     ALCORTA D.A., ERIKSON R.L.;
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::
                                    SEQUENCE
MEDLINE;
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Best Local S
Matches 1
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Best I
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ID VC
AC P1
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                                                                                                                                                                                                                                                                         LANZENDOERFER M., PALM P., GRAMPP B., PEATTIE D.A., ZILLIG W.;
NUCLEIC ACIDS RES. 20:1145-1145(1992).

-! - FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION

OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS

SUBSTRATES.

-! - CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE - N PYROPHOSPHATE +
                                                      215
                                                                                                                                                                                                                                                                                                                                                    RNA POLYMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TICKKSQGFRV-LREMHYEERATKILADVIKHQKDIEKIQELDQR-LRNHVVDPIQALHI 225
                                                                                                                                                                                                                       DIPLOMONADIDA;
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: NUCLEAR.

THREE DISTINCT ZINC-CONTAINING RNA POLYMERASES ARE FOUND IN
EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA PRECURSOR,
POLYMERASE II FOR THE MRNA PRECURSOR, AND POLYMERASE III FOR 5S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                               SHC-CLG-SARGLFLFGQPDFSYKRSNCKPIPANLQLCHGIEYQNMRLPNLLGHETMKEV
                                                      -DLLKDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (S6KII-ALPHA)
                                                                                                                                                                                                                                                                                                                                           DIFFERENT OF RNA POL
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                                                     ARCLCAAFADHSGFPFS-PNTLLDKAVCNVIASLLFACR-FEYNDPRFIRLL
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                                     Indel
                                                                                                                                                            01-MAY-1992 (REL. 22, CREATED)
01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT (EC 2 RPOA3.
GIARDIA LAMBLIA (GIARDIA INTESTINALIS).
EUKARYOTA; PROTOZOA; SARCOMASTIGOPHORA;
                   Length
                                                                                                                                                                                                                                                                                                                                          IS THE LARGEST COMPONENT (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                            -TYPE (POTENTIAL)
DCDCD942 CRC32;
          ; DB 1; LC.
6.13e-03;
Lac 21;
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2.73e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                            ZINC;
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 CRC32
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
KINASE II ALPHA 1 (EC 2.
                Score 105; DB 1
Pred. No. 6.13e-
28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSCRIPTION;
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                                                                                                                                             1741
F01949B5
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Pred. No. 2
25; Mismat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    MM;
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EMBL; X60325; G9364; -.

DNA-DIRECTED RNA POLYMERASE; T
NUCLEAR PROTEIN.

ZN_FING 79 92 C
SEQUENCE 1741 AA; 193928 MW
 XX:
                                                                                                                                                                                                                                                                                                                                        SUBUNIT: RNA POLYMERASE
SUBUNITS. THIS SUBUNIT I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.5%;
larity 27.4%;
Conservative
                 Similarity 24.7%;
18; Conservative
56683
                                                                                                                                              STANDARD;
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P18653;
01-NOV-1990 (REL. 16, C
01-NOV-1990 (REL. 16, I
01-OCT-1996 (REL. 34, I
RIBOSOMAL PROTEIN S6 K1
(P90-RSK 1).
RPS6KA1 OR RSK1.
                                                                                         228
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                                                                                         LEEESGFLPMLLN
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LEQAGAWIPLVMK
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TCEEMNDINAPYL
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20; Conse
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SUBUNIT:
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STRAIN-SSP.
MEDLINE; 92
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GIALA
                  Query Match
SEQUENCE
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P25202;
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Matches
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Matches
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                                                                                                                                                            MOL. CELL. BIOL. 9:3850-3859(1989).

-!- FUNCTION: PHOSPHORYLAIES A WIDE RANGE OF SUBSTRATES INCLUDING RIBOSONAL PROTEIN S6.

-!- TISSUE SPECIFICITY: INTESTINE, THYMUS, AND LUNG.
-!- SIMILARLY: THE N-TERMINUS SHOWS HIGH SEQUENCE SIMILARITY TO THE REGIONS OF PROTEIN KINASE C, THE CATALYTIC SUBUNIT OF CAMP-DEPENDENT PROTEIN KINASE. TH REMINDER OF S6 KINASE IS SHOWS HIGH SEQUENCE SIMILARITY TO THE CATALYTIC SUBUNIT OF PHOSPHORYLASE B KINASE.

REMINDER OF S6 KINASE IS SHOWS HORSE.

REMINDER OF S6 KINASE IS SHOWS HORSE.

REMINDER OF S6 KINASE AT S.

REMINDER OF S6 KINASE AT S.

REMINDING S6 KINASE AT S.

REMINDING S6 KINASE AT S.

REMODMAIN G6 S6 SERINE/THREONINE-PROTEIN KINASE; ATP-BINDING;

REPEAT; MULTIGENE FAMILY.

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       MAMMALIA;
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                                                                                                                           JONES
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       TETRAPODA;
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STRAIN=D;
MEDLINE; 90384864.
EFIMOV V.P., PRILIPOV A.G., MESYANZHINOV V.V.;
EFIMOV V.P., PRILIPOV A.G., MESYANZHINOV V.V.;
NUCLEIC ACIDS RES. 18:5313-5313(1990).
-!- FUNCTION: STRUCTURAL COMPONENT OF THE BASEPL!
EMBL; X15907; G15323; -.
PIR; JQ0657; G7BPT4.
-- POOTEIN.
-- POOTEIN.
-- POOTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              e 99; DB 1; L
. No. 5.67e-02;
Mismatches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ٠- کا
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nes 15
                                                                                                                           BANKSTON
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1.13e
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
PROTEIN GP7.
     VERTEBRATA;
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Pred. No. 8.
8; Mismatc
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                                                                                                                            L.J
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Pred.
13; M
                                                                                                                           SWEET
CHORDATA;
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19; Conservative
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                                                                                                                        C.M.,
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16,
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P19061;
01-NOV-1990 (REL. 16,
01-NOV-1990 (REL. 16,
01-NOV-1990 (REL. 16,
7.
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                                                                          EQUENCE FROM N.A EDLINE; 89384612
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GYRB_ACIS3 STAP
Q44273; Q60168;
01-NOV-1997 (REL.
01-NOV-1997 (REL.
DNA GYRASE SUBUNIT
GYRB.
ACINETOBACTER SP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match
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Best Local
Matches
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Matches
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                                                                                                                                                                                                        KERATIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE C.
TISSUE=LIVER;
MEDLINE; 90274676.
SATO H., KOIWAI O., TANABE K., KASHIWAMATA S.;
BIOCHEM. BIOPHYS. RES. COMMUN. 169:260-264(1990).
BIOCHEM. BIOPHYS. RES. COMMUN. 169:260-264(1990).
-!- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND INTOCENOUS COMPOUNDS.
                                                                                                                                                                                                                                                       VISION
                                                                                                                                                                                                                                                                                                                                                                                                             KNKYEDEIN-KRTECENDFVLIKKDVDEAYMNKVELEAKLESLSDEINFLRQIFEEEIR
                                                                                                         GNATHOSTOMATA;
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                                                                                                                                                                                    PREDOMINANT INTERMEDIATE
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                                                                                                                                                                                                                                                       PATTERN;
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                                                                                                                                                                                                                                                                                                                                                             520;
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                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TETRAPODA;
                                                                                                                                                                                             PATHWAY.
WITH MAMMALIAN
                                                                                                         PISCES;
ES.
 22
                                                                                                                                                                                                                                                       REPEAT
                                                                                                                                                                  ï
                                                                                                                                                                                                                                                                                                                                                                                 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                      SULT 11
UD13_RAT STANDARD; PRT; 531 AA.
Q64637;
Q1-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
Q1-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
UDP-GLUCURONOSYLTRANSFERASE 1-3 PRECURSOR, MICRC (UDPGT) (UGT1*3) (UGT1-03) (UGT1.3) (UGT13) (B3
 METLCKNDFALKI-KVKEITYINRDTKIILETKSKTIYKLN
                                                                                                                                                                                                                                                                                                                                                               -01
                        SULT 10

10N3_CARAU STANDARD; PRT; 520 AA.
P18520;
01-NOV-1990 (REL. 16, CREATED)
01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
INTERMEDIATE FILAMENT PROTEIN ON3.
CARASSIUS AURATUS (GOLDFISH).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISC OSTEICHTHYES; ACTINOPTERYGII; CYPRINIFORMES.
[1]
SEQUENCE FROM N.A.
TISSUE-GLIAL CELL;
MEDLINE; 90180470.
GIORDANO S., GLASGOW E., TESSER P., SCHECHTER NEURON 2:1507-1516(1989).
-!- FUNCTION: ONE OF THE NONNEURONAL PREDOMINA FILAMENT PROTEINS OF THE VISUAL PATHWAY.
                                                                                                                                                                                                                                                                                                                                           CRC32;
                                                                                                                                                                  SCHECHTER
                                                                                                                                                                                                                                                                                                                                                             e 96; DB 1;
No. 1.66e-
Mismatches
                                                                                                                                                                                                                                                       HEPTAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERTEBRATA;
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                                                                                                                                                                                                                                                                                                                       12
                                                                                                                                                                                                                                                                                                                                                             Score 96;
Pred. No.
14; Misma
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                                                                                                                                                                                                                                                                                                             COIL 1B.
LINKER 1
COIL 2.
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COIL 1A
LINKER
                                                                                                                                                                                                                                                      COIL;
                                                                                                                                                                                                                                                                HEAD.
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9(1995).
                                                                                                                                                                                                                                                      COILED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA;
EUTHERIA; RODENTIA.
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                                                                                                                                                                                                                                                                                                                                                             Similarity 32.2%;
19; Conservative
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420
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PROSITE; PS00226; IF;
INTERMEDIATE FILAMENT
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STRAIN-WISTAR;
MEDLINE; 95332265.
EMI Y., IKUSHIRO S
J. BIOCHEM. 117:39:
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10101100
10101010
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Best Local S
Matches
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186
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SIGNAL;
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                         ACCEPTOR
-1- CATALYTIC ACTIVITY: ...

BETA-D-GLUCORONOSIDE.

-1- SUBCELLULAR LOCATION: MICROSOMAL.

-1- SUBCELLULAR LOCATION: MICROSOMAL.

-1- ALTERNATIVE PRODUCTS: THE UGT1 GENE ENCODES FOR MANY DIFFERENT UDPGT ISOZYMES WHICH HAVE A DIFFERENT N-TERMINAL DOMAIN AND A COMMON C-TERMINAL DOMAIN OF 245 RESIDUES.

-1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY. BENEL; M34007; G207579; ALT_TERM.

R PROSITE; PS00375; UDPGT; 1.

R PROSITE; PS00375; UDPGT; 1.

R PROSITE; PS00375; UDPGT; 1.

TRANSFERASE; GLYCOSYLTRANSFERASE; GLYCOPROTEIN; TRANSMEMBRANE; SIG WULTIGENE FAMILY; MICROSOME; ALTERNATIVE SPLICING.

T GARNAMEM 489 505 POTENTIAL.

T CARBOHYD 139 139 POTENTIAL.

CARBOHYD 139 139 POTENTIAL.

CARBOHYD 293 293 POTENTIAL.

FT CARBOHYD 431 431 POTENTIAL.

CARBOHYD 531, DATENTIAL.

CARBOHYD 431 431 POTENTIAL.

CARBOHYD 431 431 POTENTIAL.
                                                                              MANY DIFFERENT
DOMAIN AND A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CREATED)
, LAST SEQUENCE UPDATE)
, LAST ANNOTATION UPDATE)
D PROTEIN IN FAA4-HOR7 INTERGENIC RECOR YM9920.01C.
SIAE (BAKER'S YEAST).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KNEFDDINSKMDRLTSNDDALTIKLNNITNEVKASYLIDDQKLEISFKL
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BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SARRELL B.G., RAJANDREAM M.A., W. TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [2]
SEQUENCE OF 950-1562 FROM N.A.
STRAIN-S288C / AB972;
GENTLES S., BOWMAN S., BARRELL B.G., RAJANDREAM M.,
SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA BANI
EMBL; Z48639; G732925; -.
EMBL; Z48756; G736313; -.
HYPOTHETICAL PROTEIN.
SEQUENCE 1562 AA; 180185 MW; CEE45672 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80
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HEMIASCOMYCETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 92; DB 1; L. Pred. No. 6.68e-01; 9; Mismatches 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
(EC 5.99.1.3) (FRAGMENTS)
                                                                                                                                                                                                                                                                                                                                                                                                                         e 94; DB 1;
No. 3.35e-
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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Pred.
15; M
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PIPANLQLCHGIEYQNM-RLP-NLLGHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YM81_YEAST STANDARD; PRT 004781; Q04029; 01-NOV-1997 (REL. 35, LAST SEQUEN 01-NOV-1997 (REL. 35, LAST SEQUEN 01-NOV-1997 (REL. 35, LAST ANNOTA HYPOTHETICAL 180.2 KD PROTEIN IN YMR247C OR YM9408.09C OR YM9920.0 SACCHAROMYCES CEREVISIAE (BAKER'S EUKARYOTA; FUNGI; ASCOMYCOTINA; H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BARRELL
                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 35.7%;
15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 38.8%;
19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-956 FROM STRAIN-S288C / AB972; HUNT S., BOWMAN S., BASUBMITTED (MAR-1995) T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , , , a
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b, , , a
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Best Loc
Matches
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Matches
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                                               MEDLINE; 97088999.

A YAMAMOTO S., HARAYAMA S.;

LINT. J. SYST. BACTERIOL. 46:506-511(1996).

-!- FUNCTION: DNA GYRASE NEGATIVELY SUPERCOLLS CLOSED CIRCULAR DOUBLE-STRANDED DNA IN AN ATP-DEPENDANT MANNER AND ALSO CATALYZES THE INTERCONVERSION OF OTHER TOPOLOGICAL ISOMERS OF DOUBLE-STRANDED DNA RINGS, INCLUDING CATENATED RINGS.

-!- CATALYTIC ACTIVITY: ATP-DEPENDENT BREAKAGE, PASSAGE AND REJOINING OF DOUBLE-STRANDED DNA.

-!- CATALYTIC ACTIVITY: ATP-DEPENDENT BREAKAGE, PASSAGE AND REJOINING OF DOUBLE-STRANDED DNA.

-!- CATALYTIC ACTIVITY: ATP-DEPENDENT BREAKAGE, PASSAGE AND REJOINING OF TWO CHAINS, THE A CHAIN IS RESPONSIBLE FOR DNA BREAKAGE AND REJOINING; THE B CHAIN CATALYZES ATP HYDROLYSIS. THE ENZYME FORMS AN A2B2 TETRAMER.

REMBL; D734421; G1322101; -.

REMBL; D734421; G1322101; -.

REMBL; D73421; G1322101; -.
                                                                                                                                                                                                                                                    DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANAEROBIC RODS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          251
                                                                                                                                  DOUBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LARRERELSFLNAGVRIVLRDERVALEHIFDLEVGLSEKSAL-DIAGLPGKLA-DCQEKD
AND COCCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
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 AEROBIC RODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SHIGELLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BANKS
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UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90; DB 1; Le:
No. 1.31e+00;
Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                         E572EEE0 CRC32
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SHIGELLA DI.

SHIGELLA DI.

PLASMID 210 KB 11.

PROKARYOTA; GRACILICUI.

ENTEROBACTERIACEAE.

[1]

SEQUENCE FROM N.A.

SPECIES-S.DYSENTERIAE; STRAIN-CG097;

YAO R., REDDY L.V., PALCHAUDHURI S.;

YAO R., REDDY L.V., PALCHAUDHURI S.;

'TTED (MAR-1991) TO EMBL/GENBANK/DDBJ DA'

"A. A. "TRAIN-2A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29, CREATED)
29, LAST SEQUENCE UPDATE)
32, LAST ANNOTATION UPDATE
TRANSCRIPTIONAL ACTIVATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YOSHIKAWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WATANABE
 SCOTOBACTERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AN C.J.;
MICROBIOL. 6:1575-1575(1992).
FUNCTION: TRANSCRIPTIONAL ACTIVATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 90;
Pred. No.
23; Misma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPEC.
YAO R., n.
SUBMITTED (MAn.
[2]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SPECIES—S.FLEXNERI; STRAIN—L.
X MEDLINE; 87032409.
SAKAI T., SASAKAWA C., MAKINO S.,
TT. IMMUN. 54:395-402(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6
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57:1391-1398(198
                                                                                                                                                                                                                                                                                                                                                                                                                                      23775 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 26.3%;
20; Conservative
PROKARYOTA; GRACILICUTES;
NEISSERIACEAE.
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY TO ARAC FAMILY MEDLINE; 92326642.
DORMAN C.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PALSELYLVEGDSAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -DINAPYLVMGQKQGG
                                                                                                                                                                                                                                                                                                                                                                                                                                         AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SAKAI T., SASAKAWA INFECT. IMMUN. 54: [3]
SEQUENCE FROM N.A. SPECIES-S.SONNEI; MEDLINE; 89212881. KATO J.I., ITO K.I INFECT. IMMUN. 57:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (REL.
(REL.
(REL.
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116
216
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Q04248;
01-JUN-1994
01-JUN-1994
01-NOV-1995
VIRULENCE RE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SHIDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             uery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DIMETHYLADENOSINE TRANSFERASE (EC 2.1.1.-) (S-ADENOSYLMETHIONINE-6-1)
N'-ADENOSYL(RRNA) DIMETHYLTRANSFERASE) (16S RRNA DIMETHYLASE) (HIGH LEVEL KASUGAMYCIN
DIMETHYLTRANSFERASE).
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      REGULON.
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N-6-METHYLTRANSFERAS
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NUCLEIC ACIDS RES. 24:4420-4449(1996).
-!- FUNCTION: SPECIFICALLY DIMETHYLATES TWO ADJACENT ADENOSINES
LOOP OF A CONSERVED HAIRPIN NEAR THE 3'-END OF 16S RRNA IN T
PARTICLE. ITS INACTIVATION LEADS TO KASUGAMYCIN RESISTANCE
(BY SIMILARITY).
-!- SIMILARITY: STRONG, TO OTHER BACTERIAL KSGA.
-!- SIMILARITY: BELONGS TO THE RRNA ADENINE N-6-METHYLTRANSFERAS FAMILY.
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ITSELF AN ACTIVATOR OF THE IPAABCD VIRULENCE
-!- SIMILARITY: BELONGS TO THE ARAC/XXLS FAMILY C
REGULATORS.

EMBL; X58464; G46954; -.

EMBL; X16661; G47067; -.

EMBL; X16661; G47067; -.

PIR; S14646; S14646.

PIR; A47605; A47605.

PIR; A60105; A60105.

PROSITE; PS00041; HTH_ARAC_FAMILY_1; 1.

PROSITE; PS01124; HTH_ARAC_FAMILY_2; 1.

PLASMID; VIRULENCE; TRANSCRIPTION REGULATION; ACT DNA_BIND

177 196 H-T-H MOTIF (BY SIMILY SEQUENCE 262 AA; 30549 MW; 11339B38 CRC32;
    IPAABCD VIRULENCE ARAC/XYLS FAMILY (
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PROSITE; PS01131; RRNA_A_DIMETH; 1.
MRNA PROCESSING; TRANSFERASE; METHYLTRANSFERASE;
ANTIBIOTIC RESISTANCE.
SEQUENCE 263 AA; 29794 MW; 357AA00D CRC32;
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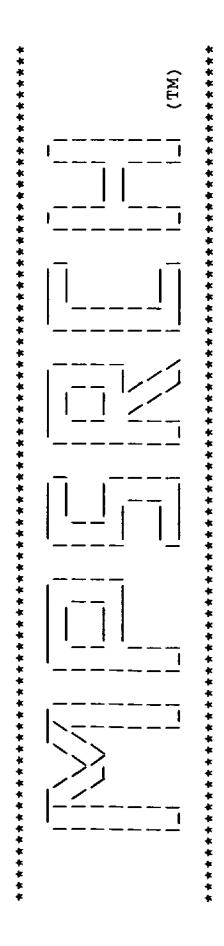
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protein database search, using Smith-Waterman algorithm protein MPsrch_pp

MasPar time 13.37 Seconds 806.104 Million cell updates/se Thu Oct 22 15:53:14 1998; Run on:

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Title: Description: Perfect Score: Sequence:

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PAM 150 Gap 11 Scoring table:

residues 36531193 120441 segs, Searched:

Post-processing

summaries 0 8 5 5 Minimum Match Listing first

pir56 1:pirl 2:pir2 3:pir3 4:pir4 Database:

0.517 scale Variance 86.902; Mean 44.927; Statistics:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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#formal_name Drosophila melanogaster
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		S. E.	o, vu ewler		., bambin; ; Nissens	, 1:; Liu, M.i.; Ainaud n, R.A.	
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 Conover,
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gene frizzled protein precursor - fruit fly (
    melanogaster)
#formal_name Drosophila melanogaster
31-Mar-1990 #sequence_revision 31-Mar-1990 #t
23-Aug-1997
S03540; S15708
S03540
Vinson, C.R.; Conover, S.; Adler, P.N.
Nature (1989) 338:263-264
A Drosophila tissue polarity locus encodes a
    containing seven potential transmembrane do
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Adler, P.N.; Vinson, C.; Park, W.J.;
Genetics (1990) 126:401-416
Molecular structure of frizzled, a D
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Pred. No. 8.11e-42;
22; Mismatches 47
  J.
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Pred. No. 8.11e-42
22; Mismatches 4
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Adler, P.N.; Vinson, C.; Park, W
Genetics (1990) 126:401-416
Molecular structure of frizzled,
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##cross-references FlyBase:FBgn0001085
trons 224/3; 264/3; 329/3; 405/1
:Y #length 415 #molecular-weight
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##cross-references FlyBase:FBgn0001085
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##molecule_type mRNA
##residues 1-581 ##label VIN
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netrin-2 precursor - chicken (fragment)

#formal_name Gallus gallus #common_name chicken

06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change

10-Sep-1997

B54665
A54665
Serafini, T.; Kennedy, T.E.; Galko, M.J.; Mirzayan, C.;
Jessell, T.M.; Tessier-Lavigne, M.

Cell (1994) 78:409-424

The netrins define a family of axon outgrowth-promoting
107
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J. Biol. Chem. (1995) 270:4705-4711
Identification of three N-terminal ends of type XVIII
collagen chains and tissue-specific differences in the expression of the corresponding transcripts. The longer form contains a novel motif homologous to rat and
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HNRCEPI -T-ISICKNIPYNMTIMPNLIGHTKQEEAGLEVHQFAPLVKIGCSDDLQLFLC
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A56101
Rehn, M.; Pihl-
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. No. 3.23e-08;
Mismatches 46
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Biochem. Biophys. Res. Commun. (1997) 235:142-147
Cloning of a mouse Smoothened cDNA and expression patterns hedgehog signalling molecules during chondrogenesis and cartilage differentiation in clonal mouse EC cells, ATDC5
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Smoothened protein - mouse
#formal_name Mus musculus #common_name house mouse
02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change
05-Sep-1997
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                                                                                                          A54665 #type complete
netrin-1 precursor - chicken
#formal_name Gallus gallus #common_name chicken
06-Jan-1995 #sequence_revision 06-Jan-1995 #text_
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##cross-references GB:L34549; NID:g529418; PID:g529419
SUMMARY #length 606 #molecular-weight 68126 #chec
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A54665
Serafini, T.; Kennedy, T.E.; Galko, Jessell, T.M.; Tessier-Lavigne, M Cell (1994) 78:409-424
The netrins define a family of axon The netrins define a family of axon
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##molecule_type mRNA
##residues 1-79
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I.; Nakazato, H.; Noguchi, T.; Sassa, S.
ochem. Blophys. Res. Commun. (1988) 156:681-688
ur species of cDNAs for cytochrome P450 isozymes
immunorelated to P450c-M/F encode for members of P450I
subfamily, increasing the number of members within the
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RAAHCEPLRYNVCLGSALPYGATT-TLLAGDSDSQEEAHGKLVLWSGLRNAPRCWAVIQP
                       KRSNCKPIPANLQLCHGIEYQNMRLPNLLGH-ETMKEVLEQAGAWIPL-VMKQCHPDTKK
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us #common_name Norway
on 27-Feb-1997 #text_c
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9
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J. Mol. Evol. (1990) 30:155-169
The rat P450 IID subfamily: complete sequences closely linked genes and evidence that gene cmaintained sequence homogeneity at the heme-bof the cytochrome P450 active site.
S16872
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NID:g203829;
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63/3; 121/1; 172/1; 225/3; 284/3; #superfamily cytochrome P450
chromoprotein; electron transfer; heme; tron; monooxygenase; oxide
                                                                                                   cytochrome P450 2D4 - rat
cytochrome P450 2D4 - rat
cytochrome P450 CMF3
#formal_name Rattus norvegicus #(
28-Feb-1990 #sequence_revision 17
23-Jan-1998
S16873; D31579
S16871
Matsunaga, E.; Umerr
J. Mol
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); NID:957815;
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##residues 1-500 ##label RES
##cross-references GB:S77859; NID:g998524; PID:g998525
##experimental_source brain, strain Sprague-Dawley
CLASSIFICATION #superfamily cytochrome P450
KEYWORDS heme; transmembrane protein
FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-Feb-1993
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Nucleic Acids Res. (1992) 20:1145

Nucleotide sequence of the gene encoding to the DNA-dependent RNA polymerase III
ces MUID:92195823
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DNA-directed RNA polymerase (EC
Giardia lamblia
#formal_name Giardia lamblia
12-Feb-1993 #sequence_revision 1
12-Sep-1997
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Lanzendoerfer, M.; Palm, P.; Gran
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#length 500 #molecular-weight
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##molecule_type DNA
##residues 1-1735 ##label LAN
##cross-references EMBL:X60325
##cross-references TABL:X60325
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Pred. No. 2
25; Mismat
                                                                                                 preliminary;
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18; Conservative
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#length 1735
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Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.
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#formal_name Methanococcus jannaschii
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, J.; Glasner,
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##residues 1-322 ##label BLAT
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Burland, V.; Riley, M.; Collado
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FIGURE

FIGURE

FINDSOMMAL Protein S6 kinase II (EC 2.7.-.-) alpha chain homolog (clone Mu6A) - mouse

ORGANISM

#formal_name Mus musculus #common_name house mouse

26-Feb-1990 #sequence_revision 31-Mar-1990 #text_change

26-Feb-1998

ACCESSIONS

AS3133

#authors

S.W.; Erikson, R.L.

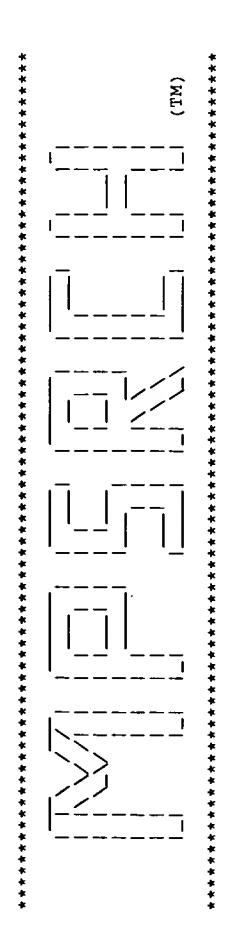
#journal

Mol. Cell. Biol. (1989) 9:3850-3859

#title

Sequence and expression of chicken and mouse rsk: homologs

*References MuID:89384612
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

- protein database search, using Smith-Waterman algorithm protein MPsrch_pp

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not generated. output Tabular

>US-08-848-439-3 (1-275) from US08848439.pep 2073 1 SARGLFLFGQPDFSYKRSNC..... Title: Description: Perfect Score: Sequence:

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. WQKGQREFKRISRSIRKLQC

PAM 150 Gap 11 Scoring table:

49795644 residues 165420 segs, Searched:

summaries 08 45 Minimum Match Listing first Post-processing:

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1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

scale 0.613 72.884; Variance Mean 44.690; Statistics:

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                                                                                                                                               TETRAPODA;
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                                                                                                                                                                                                    MAHADEVAPPA
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F ANNOTATION UPDATE
SDF5).
                                                                               CE UPDATE)
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                                                                                                                                                                                                                            DATA
                                                                                                                                                                                                                                                                                DB 11;
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I. No. 0.00e+
Mismatches
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. No. 0.00e+
Mismatches
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                                                                                                                                                                      SEQUENCE FROM N.A.
MELKONYAN H., CHANG W.C., SHAPIRO J.P., MA
FITZPATRIC P.A., KIEFER M.C., TOMEI D.L.,
SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ
EMBL; AF017989; G2415421; -.
SEQUENCE 295 AA; 33483 MW; 0E4C8A8E CR
                                                                                                                                                VERTEBRATA;
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                                                                             , LAST SEQUENCE
, LAST ANNOTATI
PROTEIN 1.
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HONJO
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LAST SEQUENTS
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2; M
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Pred.
2; M
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MEDLINE; 97092876.
SHIROZU M., TADA H., TASHIRO K
HAMADA T., SATO T., NAKANO T.,
GENOMICS 37:273-280(1996).
EMBL; D50462; G1747302; -.
MGD; MGI:108078; SDF5.
SEQUENCE 295 AA; 33501 MW;
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SULT 2
035297
035297;
035297;
01-JAN-1998 (TREMBLREL. 05, C
01-JAN-1998 (TREMBLREL. 05, L
01-AUG-1998 (TREMBLREL. 07, L
SECRETED APOPTOSIS RELATED PR(
SARP1.
MUS MUSCHIFF
                                                                                                                                              CHORDATA;
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(TREMBLREL. 03,
(TREMBLREL. 06,
L DERIVED FACTOR
                                                                                                                                                                                                                                                                              th 99.6%;
Similarity 98.9%;
272; Conservative
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86;
86;
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larity 98.9%;
Conservative
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P97299
P97299;
01-MAY-1997 (TREMBLREL.
01-JUN-1998 (TREMBLREL.
STROMAL CELL DERIVED F/SDF5.
MUS MUSCULUS (MOUSE).
FUKARYOTA; METAZOA; CF
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EUKARYOTA; METAZOA;
EUTHERIA; RODENTIA.
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les 272; Conse
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                                                                                                                                                                                                                                           HOMO SAPIENS (HUMAN).

EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMA, EUTHERIA; PRIMATES.

[1]
SEQUENCE FROM N.A.
MELKONYAN H., CHANG W.C., SHAPIRO J.P., MAHADEVAPPA M., FITZPATRIC P.A., KIEFER M.C., TOMEI D.L., UMANSKY S.R.; SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.

EMBL; AF017986; G2415415; -.
NON_TER 206 206
SEQUENCE 206 AA; 23215 MW; F465B68B CRC32;
                                                                                                                                                                                                                                                                                                                                                                  206
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
PROTEIN 1 (FRAGMENT).
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LAST ANNOTATION UPDAT
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0.00e+00;
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Pred. No. 0.00e+
0; Mismatches
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CHORDATA;
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014778
014778;
01-JAN-1998 (TREMBLREL. 05, 1
01-JAN-1998 (TREMBLREL. 05, 1
01-JAN-1998 (TREMBLREL. 05, 1
01-AUG-1998 (TREMBLREL. 07, 1
SECRETED APOPTOSIS RELATED PR
SARP1.
HOMO SAPIENC
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O14779
O14779;
O1-JAN-1998 (TREMBLREL. 05, 01-JAN-1998 (TREMBLREL. 05, 01-AUG-1998 (TREMBLREL. 07, 18 SECRETED APOPTOSIS RELATED PISARP2.
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA EUTHERIA; PRIMATES.
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05,
07,
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Similarity 98.4%;
185; Conservative
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SEQUENCE FROM 1
TISSUE=HEART;
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Best Local S
Matches 18
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PRELIMINARY; PRT; 313 AA.

000546;

01-JUL-1997 (TREMBLREL. 04, CREATED)

01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)

01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)

SECRETED FRIZZLED-RELATED PROTEIN.

HOMO SAPIENS (HUMAN).

EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MA EUTHERIA; PRIMATES.

[1]

SEQUENCE FROM N.A.

TISSUE-LUNG;

FINCH P.W., HE X., KELLEY M.J., UREN A., SCHAUDIES R.P. RUDIKOFF S., AARONSON S.A., VARMUS H.E., RUBIN J.S.;

SUBMITTED (JUN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
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 S.R.
BANKS
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                                                       e 913; DB 4; L
1. No. 3.09e-193;
Mismatches 77;
MELKONYAN H., PROCHAZKA V., CHANG W.C., UMANSKY SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA EMBL; AF017987; G2415417; -. SEQUENCE 314 AA; 35411 MW; 61E261B5 CRC32;
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ZHOU Z., WANG J.;
SUBMITTED (MAR-1998) TO EMBL/GENBANK/DDBJ
EMBL; AF001900; G2213819; -.
EMBL; AF056087; G3033551; -.
SEQUENCE 313 AA; 35314 MW; A3CD04FF CF
                                                      Score 913;
Pred. No. 3
67; Mismat
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                                MW;
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                                                      th 44.0%;
Similarity 42.6%;
112; Conservative
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larity 42.6%;
Conservative
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TISSUE=PANCREAS;
MELKONYAN H., CHANG W.C., SHAPIRO J.P., MAHADEVAPPA N
FITZPATRIC P.A., KIEFER M.C., TOMEI D.L., UMANSKY S.I
SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF017988; G2415419; -.
SEQUENCE 317 AA; 35577 MW; 2CD69373 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TETRAPODA;
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ANNOTATION UPDATE)
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE
PROTEIN 3.
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91e-1
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e-1
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426
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE=HEART;
DUPLAA C., D'AMORE P.A.;
SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ
EMBL; U85945; G2337937; -.
SIGNAL.
SIGNAL
SEQUENCE 308 AA; 34763 MW; 9B74A92F CF
                                                                                                                                                                                                                  TAURUS (BOVINE).
ARYOTA; METAZOA; CHORDATA; VERTEBRATA;
IERIA; ARTIODACTYLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
EUTHERIA; PRIMATES.
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                                                                                                            308
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Pred. No. 3
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No.
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014780;
01-JAN-1998 (TREMBLREL. 05, C. 01-JAN-1998 (TREMBLREL. 05, L. 01-JAN-1998 (TREMBLREL. 07, L. SECRETED APOPTOSIS RELATED PRC SARP3.
HOMO SAPIENC
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larity 42.2%;
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8. 8.
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O19116;
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01-JAN-1998 (TREMBLREL. 0
01-AUG-1998 (TREMBLREL. 0
FRZA PRECURSOR.
BOS TAURUS (TREMBLREL. 0
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EUTHERIA; A
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DEVELOPMENT [2]
01-AUG-1998
CRESCENT.
                            GALLIFORMES
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Best Local S
Matches 9
                                         SEQUENCE
PFEFFER P
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04, LAST SEQUENCE UPDATE)
06, LAST ANNOTATION UPDATED
1D PROTEIN SFRP-1.
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                                                                                                                                                                                                                                                                                                        Score 890; DB 11;
Pred. No. 2.10e-187;
67; Mismatches 80;
74
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Mismatches
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LAST SEQUENCE
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58;
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G1946341; -
                                                                                                                                                                                                                            CHORDATA;
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OO8861;
OO8861;
O1-JUL-1997 (TREMBLREL. 04,
O1-JUN-1998 (TREMBLREL. 06,
SECRETED FRIZZLED RELATED PI
SFRP1.
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDAT;
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Local Similarity 41.4%;
les 109; Conservative
Conservative
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SEQUENCE FROM N.A.
MEDLINE; 97250455.
RATINER A., HSIEH J.C., S
JENKINS N.A., NATHANS J.;
PROC. NATL. ACAD. SCI. U.
EMBL; U88566; G1946341; -
SFOUENCE 314 AA; 35327
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(TREMBLREL.
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C 042397;
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T 01-JAN-1998
114;
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                                                                            SEQUENCE FROM N.A.
PFEFFER P.L., IZPISUA-BELMONTE J.C., DE ROBERTIS E.M.
SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF006508; G2226372; -.
SEQUENCE 307 AA; 34683 MW; 320A2243 CRC32;
                                       ETRAPODA;
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                                                                                                                                               ; DB 13; L
8.17e-147;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE
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Pred. No. 3.03e-110;
65; Mismatches 101;
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ANNOTATION
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                                       VERTEBRATA;
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VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              281
                                                                                                                                                         Score 729;
Pred. No. 8
68; Mismat
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LAST
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SEQUENCE FROM N.A.
MEDLINE; 98088686.
                                     CHORDATA;
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SALIC A.N., KROLL K.L., EVA
SUBMITTED (APR-1998) TO EME
EMBL; AF059570; G3089551; -
SEQUENCE 281 AA; 31834 M
                                                                                                                                                        similarity 35.2%;
96; Conservative
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Local Similarity 32.7%;
nes 86; Conservative
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O73821;
O1-AUG-1998 (TREMBLREL. 0
01-AUG-1998 (TREMBLREL. 0
01-AUG-1998 (TREMBLREL. 0
SECRETED XWNT8 INHIBITOR
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                                                                                                                                                                                                                                                                      [1]
SEQUENCE FROM N.A.
MEDLINE; 96224032.
MEDLINE; 96224032.
MANG Y., MACKE J.P., ABELLA B.S., ANDREASSON K., WORLEY P.
GILBERT D.J., COPELAND N.G., JENKINS N.A., NATHANS J.;
J. BIOL. CHEM. 271:4468-4476(1996).
EMBL; U43320; G1151258; -.
MGD; MGI:108570; FZD7.
AGD; MGI:108570; FZD7.
AGD: MGI:108570; FZD7.
SEQUENCE 572 AA; 63816 MW; FA1D78D2 CRC32;
SEQUENCE 572 AA; 63816 MW; FA1D78D2 CRC32;
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                                                                                                                                      RESULT 14

ID Q61090

AC Q61090;

AC Q61090;

DT Q1-NOV-1996 (TREMBLREL. 01, CREATED)

DT O1-NOV-1996 (TREMBLREL. 05, LAST SEQUENCE UPDATE)

DT O1-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)

DT O1-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)

DF FRIZZLED HOMOLOG 7 (TRANSMEMBRANE RECEPTOR).

GN FZD7 OR FRIZZLED 7.

OS MUS MUSCULUS (MOUSE).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; M
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Pred. No. 4.11e-65
25; Mismatches 4
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1. No. 1.23e-6
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Pred. No. 1
32; Mismat
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G1906598; -.
AA; 64466 MW; 8
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MEDLINE; 97227293.
WANG Y.K., HARRYMAN S
FRANCKE U.;
HUM. MOL. GENET. 6:46
EMBL; U82169; G190659
SEQUENCE 591 AA; 6
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01-JUL-1997 (TREM
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FZD3.
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-VCEACKNKND--DDNDIMETLCKNDFALKIKVKEITYINRDTKIIL
                       ETEGPVEFIKQGLLLPYDTRTMIEQWLLINENCAQKLIRTRPTVYVIAGEIHHGKVKVNR
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)TA; METAZOA; CHORDATA; VERTEBRATA;
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CAENORHABDITIS ELEGANS.
EUKARYOTA; METAZOA; ACOELOMATES; NI
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Pred.
25; M
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SEQUENCE FROM N.A.
TISSUE-LIMB BUD;
KENGAKU M., TWOMBLY V., TABIN C
COLD SPRING HARB. SYMP. QUANT.
EMBL; AF031830; G2655274; -.
TRANSMEMBRANE.
SEQUENCE 592 AA; 65490 MW;
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nes 49; Conservative
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7-TRANSMEMBRANE PROTEIN F
FZ-1.
GALLUS GALLUS (CHICKEN).
EUKARYOTA; METAZOA; CHORD
SOHLLPATEEAPK
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

search, using Smith-Waterman algorithm protein database protein MPsrch_pp

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>US-08-848-439-3 (1-275) from US08848439.pep 2073 1 SARGLFLFGQPDFSYKRSNC....

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Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

120441 seqs, 36531193 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pirl 2:pir2 3:pir3 4:pir4 5:nrl3d

0.508 scale Variance 87.725; Mean 44.556; Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	1.05e-51		1.19e-45	ო	m.	.96	.04e-0	.87e-0	.66	.94e-0	.34	.97e-0	3.97e-01	.34e-0	.17	.17e-0	.62e-0	.29e+0	7	29	3.04e+00	.03e+0	4.03e+00
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ACCESSI REFEREN	ESSIONS ERENCE #authors	A45054 A45054 Chan, 8 M.S.,	S.D.	Ka ng,	pf, D.B.; F V.; Bambino	es, M.E.; ; Liu, M.	Hooks, M.; Y.; Arnaud,	Bradley, C.D.;
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SUMMARY Query Best Match	Match Local S es 4	#leng imilarity 9; Cons	gth 641 18. ty 39. servati	# (0 00 00 (0 00 00	olecular-we Score 386; Pred. No. 27; Misma	ght 71054 # DB 2; Leng .05e-51; ches 43; I	checksum 83 th 641; ndels 6;	sd
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Db 1	66 SMY :: 77 SLF	APVC-TVLI APVCLDDLI	EQALPPC :::: DETIQPC	RSL :	CERAQG-CEALMNK) : : : CVQVKDRCAPVMSA)	NKFGFQWPDTLKC:	EKFPVHGRGELC ::[: DRFP-QD-NDLC	CVG 223 : CIP 134
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hypothetical protein - fruit fly (Drosophila
#formal_name Drosophila melanogaster
21-Nov-1993 #sequence_revision 10-Nov-1995
16-Feb-1997
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dfz2 protein - fruit fly (Drosophila melan

#formal_name Drosophila melanogaster

12-Feb-1998 #sequence_revision 13-Mar-1998

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Bhanot, P.; Brink, M.; Harryman Samos, C.
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Y.; Macke, J.P.; Andrew, D.; Nathans,
Nature (1996) 382:225-230
A new member of the frizzled family from
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Pred. No. 1.19e-45;
32; Mismatches 45
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Pred. No. 1.19e-45,
32; Mismatches 4:
                      Nathans, J.
Data Library
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#molecule_type DNA
#residues 1-694 ##label BHA
#cross-references EMBL:U65589
#length 694 #molecular-we
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#cross-references EMBL:U65589
#length 694 #molecular
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Bhanot, P.
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                       Drosophila
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#formal_name Drosophila melanogaster
31-Mar-1990 #sequence_revision 31-Mar-1990 #t
23-Aug-1997
S03540
S03540
Vinson, C.R.; Conover, S.....
Nature (1989) 220
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Adler, P.N.; Vinson, C.; Park, W.J.;
Genetics (1990) 126:401-416
Molecular structure of frizzled, a D:
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Pred. No. 3.34e-41;
22; Mismatches 47
Adler, P.N.; Vinson, C.; Park, W.J
Genetics (1990) 126:401-416
Molecular structure of frizzled, a
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Pred. No. 3.34e-41
22; Mismatches 4
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Nature (1989) 338:263-264
A Drosophila tissue polarity locus
containing seven potential trans
ces MUID:89159415
                                                                                                                        ne FlyBase:fz
##cross-references FlyBase:FBgn0001085
trons 224/3; 264/3; 329/3; 405/1
X #length 415 #molecular-weight
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##cross-references FlyBase:FBgn0001085
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#residues
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#accession S15709
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                                                                                                                                          collagen alpha 1(XVIII) chain precursor long form - mouse (fragment)
#formal_name Mus musculus #common_name house mouse 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 10-Sep-1997
B56101
A56101
Rehn, M.; Pihlajaniem*
J. Biol
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J. Biol. Chem. (1995) 270:4705-4711

Identification of three N-terminal ends of type XVIII

collagen chains and tissue-specific differences in the
expression of the corresponding transcripts. The longes
form contains a novel motif homologous to rat and

brosophila frizzled proteins.
                                           76
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                         B54665  #type fragment
netrin-2 precursor - chicken (fragment)
#formal_name Gallus gallus #common_name chicken
06-Jan-1995 #sequence_revision 06-Jan-1995 #text_chi
10-Sep-1997
B54665
A54665
Serafini, T.; Kennedy, T.E.; Galko, M.J.; Mirzayan,
Jessell, T.M.; Tessier-Lavigne, M.
Cell (1994) 78:409-424
The netrins define a family of axon outgrowth-promot
proteins homologous to Caenorhabditic - septembly of axon outgrowth and a family of axon outgrowth a family of axon outgrowth a family of axon outgrowth and a family of axon outgrowth a f
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erences GB:L34550; NID:g529420; PID:g5294
#length 581 #checksum 7731
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. No. 4.04e-08;
Mismatches 46;
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30; Conservative
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JC5539 #type complete
Smoothened protein - mouse
#formal_name Mus musculus #common_name house mouse
02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change
05-Sep-1997
JC5539; PC4476
JC5539
Akiyama, H.; Shigeno, C.; Hiraki, Y.; Shukunami, C.; Kohno, H.; Akagi, M.; Konishi, J.; Nakamura, T.
Biochem. Biophys. Res. Commun. (1997) 235:142-147
Cloning of a mouse Smoothened cDNA and expression patterns of hedgehog signalling molecules during chondrogenesis and cartilage differentiation in clonal mouse EC cells, ATDC5.
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netrin-1 precursor - chicken
#formal_name Gallus gallus #common_name chicken
06-Jan-1995 #sequence_revision 06-Jan-1995 #text_ch
10-Sep-1997
A54665
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Serafini, T.; Kennedy, T.E.; Galko, M.J.; Mirzayan,
Jessell, T.M.; Tessier-Lavigne, M.
Cell (1994) 78:409-424
The netrins define a family of axon outgrowth-promo
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Mismatches 41;
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##residues 528-533;539-545;600-605 ##1
##experimental_source ADTC5 cell
##experimental_source ADTC5 cell
IT This protein is used in the conserved
Signalling pathway, together with Pa
are responsible for the skeletal abn
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hypothetical protein b0872 - Escherichia coli (strain K
#formal_name Escherichia coli
12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change
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Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna,
Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna,
Burland, V.; Riley, M.; Collado-Vides, J.; Glasner,
Rode, C.K.; Mayhew, G.F.; Gregor, J.; Davis, N.W.;
Rode, C.K.; Mayhew, G.F.; Gregor, J.; Davis, B.
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cytochrome P450 2D4 - rat
cytochrome P450 2D4 - rat
cytochrome P450CMF3
#formal_name Rattus norvegicus #common_name Norway rat
28-Feb-1990 #sequence_revision 17-May-1996 #text_change
23-Jan-1998
S16873; D31579
S16871
Matsunaga, E.; Umeno, M.; Gonzalez, F.J.
J. Mol. Evol. (1990) 30:155-169
The rat P450 IID subfamily: complete sequences of four
closely linked genes and evidence that gene conversions
maintained sequence homogeneity at the heme-binding region
of the cytochrome P450 active site.
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I.; Nakazato, H.; Noguchi, T.; Sassa, S.
Biochem. Biophys. Res. Commun. (1988) 156:681-688
Four species of cDNAs for cytochrome P450 isozymes
immunorelated to P450c-M/F encode for members of P4
subfamily, increasing the number of members within
subfamily.
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oxidoreductase; 
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                                 substrain MG1655
-weight 35740 #ch
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                                                                                       Score 99; DB 2; Les
Pred. No. 5.34e-01;
22; Mismatches 21;
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Pred. No. 3.97e-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63/3; 121/1; 172/1; 225/3; 284/3; #superfamily cytochrome P450 chromoprotein; electron transfer; heme; iron; monooxygenase; oxido
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ISH
NID:9203829;
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-references EMBL:X52029; NID:g57815;
A90151
Ishida, N.; Tawaragi, Y.; Inuzuka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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   predicted
#length 500 #molecular-weigh
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2D4 - rat
                                   rain K-12,
#molecular-
GB:AE000189;
UWGP:b0872
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                                  ##experimental_source strain SUMMARY #mole
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#accession D31579
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P450 2
                                                                                        4.8%;
larity 27.5%;
Conservative
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larity 26.7%;
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##residues 1-5
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sion S16873
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                  rat
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#text_chang
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cytochrome P450 2D4 homolog, brain (clone 2d-29) - re
cytochrome P450 2D4 homolog, brain (clone 2d-29) - re
#formal_name Rattus norvegicus #common_name Norway re
27-Feb-1997 #sequence_revision 27-Feb-1997 #text_char
23-Jan-1998
I52313
I52313
Kawashima, H.; Strobel, H.W.
Blochem. Blophys. Res. Commun. (1995) 209:535-540
cDNA cloning of a novel rat brain cytochrome P450 be:
to the CYP2D subfamily.
ferences MUID:95251650
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protein kinase ATP-binding motify
protein kinase homology #label Ki
#molecular-weight 81594 #checks
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 #type complete
ribosomal protein S6 kinase II (EC 2.7.-.-)
homolog (clone Mu6A) - mouse
#formal_name Mus musculus #common_name house
31-Mar-1990 #sequence_revision 31-Mar-1990 #
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                                                                                                                                                                                        ##residues 1-500 ##label RES
##cross-references GB:S77859; NID:g998524; PID:g999
##experimental_source brain, strain Sprague-Dawley
CLASSIFICATION #superfamily cytochrome P450
KEYWORDS heme; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alcorta, D.A.; Crews, C.M.; Sweet, L.J. S.W.; Erikson, R.L.
Mol. Cell. Biol. (1989) 9:3850-3859
Sequence and expression of chicken and Xenopus laevis ribosomal S6 kinase.
                                                                                                                                                                                                                                                                                                                       Score 100; DB 2; L. Pred. No. 3.97e-01; 22; Mismatches 18;
                                                                                                                                                                                                                                                                                               #molecular-weight 56683
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1. No. 5.34e-01;
Mismatches 18
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th 500 #molecular-weig]
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N #superfamily ribosomal
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larity 35.2%;
Conservative
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16; Conservative
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Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, J.A.; FitzGerald, L.M.; Clayton, R.A.; Gocayne, J.D.; Kerlavage, A.R.; Dougherty, B.A.; Tomb, J.F.; Adams, M.D.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Scott, J.L.; Geoghagen, N.S.M.; Weidman, J.F.; Fuhrmann, J.L.; Nguyen, D.; Utterback, T.R.; Kelley, J.M.; Peterson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.; Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.R.; Venter, J.C. Science (1996) 273:1058-1073
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hypothetical protein MJ1398 - Methanococcus #formal_name Methanococcus jannaschii 13-Sep-1996 #sequence_revision 13-Sep-1996 # A64474 A64300
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. No. 7.17e-01;
Mismatches 14
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#length 391 #molecular-weight
                                                                                                                                                                                                                                                                                                                                                                                   preliminary; nucleic acid translation not shown
                                                                                                                                                                                                                                                                                                               Complete genome sequence of Methanococcus jannaschil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 98;
Pred. No. 7
19; Mismat
                                                                                                                                                                                                                                                                                                                                                                                                                                 1-391 ##label BUL
es GB:U67580; GB:L'
TIGR:MJ1398; PI
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                                                                                                                                                                                                                                                                                                                                                                                                                   ##molecule_type DNA
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REFERENCE
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Unit. Release 3.1A John F. Collins, Biocomputing Research Copyright (c) 1993-1998 University of Edinburgh, U. Distribution rights by Oxford Molecular Ltd - protein database search, using Smith-Waterman algorithm protein MPsrch_pp

MasPar time 18.49 Seconds 794.551 Million cell updates/sec Thu Oct 22 15:51:29 1998; Run on:

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>US-08-848-439-2 (1-295) from US08848439.pep 2234 Title: Description: Perfect Score: Sequence:

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295

PAM 150 Gap 11 Scoring table:

49795644 residues 165420 seqs, Searched:

Minimum Match 0% Listing first 45 Post-processing

summaries

Database:

sptrembl6
1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

scale 0.633 Variance 71.230; Mean 45.109; Statistics:

No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, a derived by analysis of the total score distribution. Pred. No. score grea and is der

SUMMARIES

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PROTEIN 1.
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          PRELIMINARY; PRT; 295 AA.
035297;
01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UP
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION
SECRETED APOPTOSIS RELATED PROTEIN 1.
SARP1.
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TE
EUTHERIA; RODENTIA.
[1]
SEQUENCE FROM N.A.
MELKONYAN H., CHANG W.C., SHAPIRO J.P., MAHA
FITZPATRIC P.A., KIEFER M.C., TOMEI D.L., UM
SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DA
EMBL; AF017989; G2415421; -.
SEQUENCE 295 AA; 33483 MW; OE4C8A8E CRC3
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MEDLINE; 97092876.
SHIROZU M., TADA H., TASHIRO K
HAMADA T., SATO T., NAKANO T.,
GENOMICS 37:273-280(1996).
EMBL; D50462; G1747302; -.
MGD; MGI:108078; SDF5.
SEQUENCE 295 AA; 33501 MW;
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TO P97299

NC P97299;

NT 01-MAY-1997 (TREMBLREI)

NT 01-JUN-1998 (TREMBLREI)

SE STROMAL CELL DERIVED IS

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MUS MUSCULUS (MOUSE).

CEUKARYOTA; METAZOA; CH
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O14778

O14778;

O14778;

O1-JAN-1998 (TREMBLREL. 05, CREATED)

O1-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)

O1-JAN-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)

SECRETED APOPTOSIS RELATED PROTEIN 1 (FRAGMENT).

SARP1.

HOMO SAPIENS (HUMAN).

EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMELYARYOTA; PRIMATES.

[1]

SEQUENCE FROM N.A.

MELKONYAN H., CHANG W.C., SHAPIRO J.P., MAHADEVAPPA M., FITZPATRIC P.A., KIEFER M.C., TOMEI D.L., UMANSKY S.R.; SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.

EMBL; AF017986; G2415415; -.

NON_TER 206 206

SEQUENCE 206 AA; 23215 MW; F465B68B CRC32;
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O14779;
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01-JAN-1998 (TREMBLREL. 05, I
01-AUG-1998 (TREMBLREL. 07, I
SECRETED APOPTOSIS RELATED PI
SARP2.
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA
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[1]
SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BANK
                                                                                                                                                                                                                                                                                                                                                                                                        O00546 PRELIMINARY; PRT; 313 AA.
O00546;
O1-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
O1-JUL-1998 (TREMBLREL. 07, LAST ANNOTATION UPDAT)
SECRETED FRIZZLED-RELATED PROTEIN.
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPOI
                                                                              .99;
77;
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Pred. No. 8.79e-199;
67; Mismatches 77;
  UMANSKY
MELKONYAN H., PROCHAZKA V., CHANG W.C., UMANSKY SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA EMBL; AF017987; G2415417; -. SEQUENCE 314 AA; 35411 MW; 61E261B5 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
ZHOU Z., WANG J.;
SUBMITTED (MAR-1998) TO EMBL/GENBANK/DDBJ DATA
EMBL; AF001900; G2213819; -.
EMBL; AF056087; G3033551; -.
SEQUENCE 313 AA; 35314 MW; A3CD04FF CRC32;
                                                                 Score 913; DB 4;
Pred. No. 2.63e-1
67; Mismatches
                                                                                                                                                                                                                                                                                                                                        306
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larity 42.6%;
Conservative
                                                                th Similarity 42.6%; 112; Conservative
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TISSUE-LUNG;
FINCH P.W., HE X.,
RUDIKOFF S., AARONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIMATES
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112; Conse
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Best Local S
Matches 11
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                                                                                                                                                                                                                                       TETRAPODA;
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SEQUENCE FROM N.A.
TISSUE=PANCREAS;
MELKONYAN H., CHANG W.C., SHAPIRO J.P., MAHADEVAPPA
FITZPATRIC P.A., KIEFER M.C., TOMEI D.L., UMANSKY S.
SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
EMBL; AF017988; G2415419; -.
SEQUENCE 317 AA; 35577 MW; 2CD69373 CRC32;
SEQUENCE 317 AA; Lengt
                                                                                                                                           CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
PROTEIN 3.
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1. No. 2.00e-196;
Mismatches 79;
                                                                                                                                                                                                                                                                                                                                                   DATA
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Pred.
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; METAZOA; CHORDATA;
ARTIODACTYLA.
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014780;
014780;
01-JAN-1998 (TREMBLREL. 05,
01-JAN-1998 (TREMBLREL. 05,
01-AUG-1998 (TREMBLREL. 07,
SECRETED APOPTOSIS RELATED P.
SARP3.
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
EUTHERIA; PRIMATES.
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 IHKWDKKNKEFKNFMKKMKNHEC
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Similarity 42.2%;
111; Conservative
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34763
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TISSUE=HEART;
DUPLAA C., D'AMORE P.A.;
SUBMITTED (JAN-1997) TO EI
EMBL; U85945; G2337937; -
                                                                                                           PRELIMINARY
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(TREMBLREL.
(TREMBLREL.
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01-JAN-1998 (TR)
01-AUG-1998 (TR)
FRZA PRECURSOR.
BOS TAURUS (BOV:
EUKARYOTA; META!
EUTHERIA; ARTIO!
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019116;
01-JAN-1998
01-JAN-1998
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Best Local S
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01-AUG-1998 (TREMBLREL.
CRESCENT.
GALLUS GALLUS (CHICKEN).
EUKARYOTA; METAZOA; CHOR
GALLIFORMES.
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96; Conse
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073821
073821;
01-AUG-1998
01-AUG-1998
01-AUG-1998
SECRETED XWN
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                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                             SULT 9
008861
008861;
008861;
01-JUL-1997 (TREMBLREL. 04, CREATED)
01-JUL-1997 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
SECRETED FRIZZLED RELATED PROTEIN SFRP-1.
SFRP1.
MUS MUSCULUS (MOUSE).
EUTHERIA; RODENTIA.
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                                74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 890; DB 11;
Pred. No. 2.76e-19
67; Mismatches 8
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                                Mismatches
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LAST SEQUENCE
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                               58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [1]
SEQUENCE FROM N.A.
MEDLINE; 97250455.
RATTNER A., HSIEH J.C., SMALLWO
JENKINS N.A., NATHANS J.;
PROC. NATL. ACAD. SCI. U.S.A. 9
EMBL; U88566; G1946341; -.
SEQUENCE 314 AA; 35327 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29
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Similarity 41.4%;
109; Conservative
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                               Conservative
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042397
042397;
01-JAN-1998
01-JAN-1998
                               114;
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                                   TETRAPODA;
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BANKS
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                                                                                  ROBERTIS E.
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                                                                                                                                          e 729; DB 13; L
1. No. 2.17e-151;
Mismatches 94;
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07, LAST SEQUENCE UPDATE)
07, LAST ANNOTATION UPDAT
 UPDAT
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Pred. No. 1.20e-113;
65; Mismatches 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Σ
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[2]
SEQUENCE FROM N.A.
SALIC A.N., KROLL K.L., EVANS L.M., KIRSCHNER M SUBMITTED (APR-1998) TO EMBL/GENBANK/DDBJ DATA EMBL; AF059570; G3089551; -
SEQUENCE 281 AA; 31834 MW; 8478D86B CRC32;
                                                                                                                     CRC32
 ANNOTATION
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                                                          [1]
SEQUENCE FROM N.A.
PFEFFER P.L., IZPISUA-BELMONTE J.C., DE RC
SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ
EMBL; AF006508; G2226372; -.
SEQUENCE 307 AA; 34683 MW; 320A2243 CI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SZL.
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
[1]
                                   VERTEBRATA;
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MEDLINE; 98088686.
SALIC A.N., KROLL K.L., EVANS L.M.,
DEVELOPMENT 124:4739-4748(1997).
                                                                                                                                            Score
Pred.
68; M
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SIZZLED.
                                   CHORDATA;
                                                                                                                                          32.6%;
larity 35.8%;
Conservative
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86; Conservative
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LDDLDETIQPCHSLCVQVKDRCAPVMSAFGFPWPDMLECDRFP-QDN-DLCIPLASSD
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                                                                                                                                                                                                CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              e 396; DB 11;
. No. 4.38e-67;
Mismatches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 394; DB 4;
Pred. No. 1.35e-6
32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERTEBRATA;
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Pred. No. 4
25; Mismat
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MEDLINE; 97227293.
WANG Y.K., HARRYMAN SAMOS C., PEOP FRANCKE U.;
HUM. MOL. GENET. 6:465-472(1997).
EMBL; U82169; G1906598; -.
SEQUENCE 591 AA; 64466 MW; 88C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHORDATA;
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48; Conservative
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(TREMBLREL.
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EUKARYOTA; METAZOA;
EUTHERIA; PRIMATES.
                                                                                                                                                      164
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000144;
01-JUL-1997
01-JUL-1997
01-JAN-1998
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EMBL; AF013953; G2463674; -
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Unit Release 3.1A John F. Collins, Biocomputing Research Copyright (c) 1993-1998 University of Edinburgh, U.
Distribution rights by Oxford Molecular Ltd

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:part2 3:part3 4:part4 5:part5 6:part6 7:part7
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scale 0.253 Variance 130.530; 33.049; Mean Statistics

No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, derived by analysis of the total score distribution. Pred. No. score grea and is der

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	_	Pred. No.
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ALIGNMENT

This protein comprises the mouse transmembrane receptor,

This protein comprises the mouse transmembrane receptor,

frizzled-7 (Mfz7), encoded by the Mfz7 gene (see T89891). It is

an example of a Wnt receptor. Other novel frizzled family members

have been identified in human, mouse and Caenorhabditis elegans

c see W31268-74) and are considered also to be Wnt receptors. Wnt

receptors can be used in a novel, claimed method of screening for

compounds which modulate the binding of a Wnt polypeptide (secreted

proteins involved in cell-to-cell signalling) to a Wnt receptor.

Wnt is involved in (mammary) cancer and other processes involving

growth, development and proliferation (both normal and abnormal).

Modulators identified by the claimed method are useful for

treatment of diseases related to these conditions. binding modulators - useful for development or proliferation related stein; Mfz7 gene;
growth; cell proliferation b r. J, Nathans receptor). 7 protein; cell growt JUNIOR. Hsieh J (Wnt ¥ Whit is signal transduct.

Signal transduct.

Mus musculus.

WO9739357-A1.

23-OCT-1997.

11-APR-1997; U06049.

12-APR-1996; US-015307.

(UYJO) UNIV JOHNS HOPKINS.

(STRD) UNIV LELAND STANFORD JU
Andrew D, Bhanot P, Brink M, H&
I Nusse R, Samos CH, Wangy;

R WPI; 97-526631/48.

R PSDB; T89891.

I dentification of Whit receptor

Treatment of cancer and growth it receptor and growth, Mouse frizzled-7 protein Mfz7 Wnt receptor; mouse frizzled-7 signal transduction; cancer; co 572 entry) Protein; (first LT 1 W31273 standard; E W31273; 27-APR-1998 (firs Mouse frizzled-7 E Sequence RESULT

Gaps ŝ Length 572; Indels DB 27; L/ 11e-28; Score 396; DB 2 Pred. No. 2.11e-25; Mismatches Similarity 40.7%; 48; Conservative Match Local Query Ma Best Loc Matches

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ف
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Nusse R. Samos CH. Wangy:

Nusse R. Samos CH. Wangy:

WPI; 97-526631/48.

N-PSDB; T89892.

Identification of Wnt receptor binding modulators - useful for treatment of cancer and growth, development or proliferation related disorders

Disclosure; Page 48-50; 61pp; English.

This protein comprises the mouse transmembrane receptor,

This protein comprises the mouse and Caenorhabditis elegans

(see W31268-74) and are considered also to be Wnt receptors. Wnt receptors can be used in a novel, claimed method of screening for compounds which modulate the binding of a Wnt polypeptide (secreted proteins involved in cell-to-cell signalling) to a Wnt receptor.

Wnt is involved in (mammary) cancer and other processes involving growth, development and proliferation (both normal and abnormal).

Modulators identified by the claimed method are useful for treatment of diseases related to these conditions.
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27-APR-1998 (first entry)
Human frizzled-5 protein Mfz5 (Wnt receptor).
Wnt receptor; human frizzled-5 protein; Hfz5 gene; signal transduction; cancer; cell growth; cell prolif Homo sapiens.
W09739357-A1.
23-OCT-1997.
11-APR-1997; U06049.
12-APR-1996; US-015307.
(UYJO ) UNIV JOHNS HOPKINS
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This protein comprises the human transmembrane receptor,

frizzled-5 (Hfz5), encoded by the Hfz5 gene (see T89889). It is

an example of a Wnt receptor. Other novel frizzled family members

have been identified in human, mouse and Caenorhabditis elegans

(see W31268-74) and are considered also to be Wnt receptors. Wnt

receptors can be used in a novel, claimed method of screening for

compounds which modulate the binding of a Wnt polypeptide (secreted

proteins involved in cell-to-cell signalling) to a Wnt receptor.

Wnt is involved in (mammary) cancer and other processes involving

growth, development and proliferation (both normal and abnormal).

Modulators identified by the claimed method are useful for

treatment of diseases related to these conditions.
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This protein comprises the mouse transmembrane receptor,

frizzled-4 (Mfz4), encoded by the Mfz4 gene (see T89888). It is
an example of a Wnt receptor. Other novel frizzled family members
have been identified in human, mouse and Caenorhabditis elegans
(see W31268-74) and are considered also to be Wnt receptors. Wnt
receptors can be used in a novel, claimed method of screening for
compounds which modulate the binding of a Wnt polypeptide (secreted
proteins involved in cell-to-cell signalling) to a Wnt receptor.
Wnt is involved in (mammary) cancer and other processes involving
growth, development and proliferation (both normal and abnormal).
Modulators identified by the claimed method are useful for
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27-APR-1998 (first entry)
Mouse frizzled-4 protein Mfz4 (W
Wnt receptor; mouse frizzled-4 p
signal transduction; cancer; cel
Mus musculus.
W09739357-A1.
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larity 38.8%;
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7-526631/48.
7-1-100 of
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Nusse R, Samos CH, Wangy;

Nusse R, Samos CH, Wangy;

N-PSDB; T89887.

Identification of Wnt receptor binding modulators - useful for treatment of cancer and growth, development or proliferation related disorders

T treatment of cancer and growth, development or proliferation related disorders

Disclosure; Page 30-31; 61pp; English.

This protein comprises the Caenorhabditis putative transmembrane receptor, frizzled-1, encoded by the Cfzl gene (see T89887). It is an example of a wnt receptor. Other novel frizzled family members have been identified in human, mouse and Caenorhabditis elegans (see W31268-74) and are considered also to be Wnt receptors. Wnt receptors can be used in a novel, claimed method of screening for compounds which modulate the binding of a Wnt polypeptide (secreted proteins involved in cell-to-cell signalling) to a Wnt receptor.

Wnt is involved in (mammary) cancer and other processes involving growth, development and proliferation (both normal and abnormal).

Modulators identified by the claimed method are useful for treatment of diseases related to these conditions.
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                                                                                                                                                                                                            Caenorhabditis frizzled-1 protein Cf21 (Wnt receptor).
Wnt receptor; Caenorhabditis frizzled-1 protein; Cf21 gene;
Signal transduction; cancer; cell growth; cell proliferation.
Caenorhabditis elegans.
W09739357-A1.
23-OCT-1997.
11-APR-1997; U06049.
12-APR-1996; US-015307.
(UYJO ) UNIV JOHNS HOPKINS.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Andrew D, Bhanot P, Brink M, Hsieh J, Nathans J,
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larity 38.3%;
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Drosophila frizzled-2 protein (Wnt receptor).
Wnt receptor; Drosophila frizzled-2 protein; Dfz2 gene
wingless receptor; Wg receptor; signal transduction; co
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Hsieh J
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11-APR-1997; U06049.
12-APR-1996; US-015307.
(UYJO) UNIV JOHNS HOPKINS.
(STRD) UNIV LELAND STANFORD JANGREW D, Bhanot P, Brink M, Hinusse R, Samos CH, Wangy; WPI; 97-526631/48.
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S Disclosure; Page 27-29; 61pp; English.

C This protein comprises the mouse frizzled-3 protein encoded by the Mf23 gene (see T89886), and is a Wht receptor. Other novel trizzled family members have been identified in human, mouse and caenorhabditis elegans (see W31268-74) and are considered also to be Wht receptors. What receptors can be used in a novel, claimed method of screening for compounds which modulate the binding of a what polypeptide (secreted proteins involved in cell-to-cell what polypeptide (secreted proteins involved in (mammary) cancer and other processes involving growth, development and proliferation (both normal and abnormal). Modulators identified by the claimed content of diseases related to these
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1. No. 2.03e-20;
Mismatches 54;
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cell growth
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W31272 standard; Protein,
W31272;
27-APR-1998 (first entry)
Mouse frizzled-6 protein Mfz6 (Wr
ynal transduction; cancers musculus.
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W09739357-A1.

23-OCT-1997.

11-APR-1997; U06049.

12-APR-1996; US-015307.

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AArew D, Bhanot P, Brink M, Hi
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Nusse R, Samos CH, Wangy
WPI; 97-526631/48.
N-PSDB; T89890.
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disorders
Disclosure; Page 41-42;
This protein comprises t
frizzled-6 (Mfz6), encod
an example of a Wnt rece
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Identification
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have been identified in human, mouse and Caenorhabditis elegans (see W31268-74) and are considered also to be Wnt receptors. Wnt receptors can be used in a novel, claimed method of screening for compounds which modulate the binding of a Wnt polypeptide (secreted proteins involved in cell-to-cell signalling) to a Wnt receptor. Wnt is involved in (mammary) cancer and other processes involving growth, development and proliferation (both normal and abnormal). Modulators identified by the claimed method are useful for treatment of diseases related to these conditions.
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Claim 1; Page 48-50; 58pp; English.
An E10 chick brain cDNA library was screened with probes based cnetrin-1 (p78) or netrin-2 (p75) sequences to isolate chick p78 netrin-1 (p78) or netrin-2 (p75) sequences to isolate chick p78 and p75 partial cDNA clones. Full-length clones (given in and p75 partial cDNA clones. Full-length clones (given in Q92366-67, respectively) were subsequently obtd. by 3'RACE. cD1 Q92366-67, respectively) were subsequently for recombinant p78 and continessed e.g. in COS or insect cells for recombinant p78 and continessed e.g. in COS or insect cells for recombinant p78 and continessed e.g. in COS or insect cells for recombinant p78 and continessed e.g. in COS or insect cells for recombinant p78 and continessed e.g. in COS or insect cells for recombinant p78 and continessed e.g. in COS or insect cells for recombinant p78 and continessed e.g. in COS or insect cells for recombinant p78 and continessed e.g. in COS or insect cells for recombinant p78 and continessed e.g. in COS or insect cells for recombinant p78 and continessed e.g. in COS or insect cells for recombinant p78 and continessed e.g. in COS or insect cells for recombinant p78 and continessed e.g. in COS or insect cells for animals.
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disease; transgenic animal;
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netrin-2; p75; neurodegenerative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neural axon out-growth modulators derived from EGF-like repeats on netrin 1 or netrin 2 - comprise peptide(s) capable of selectively increasing spinal axon out-growth or directing axon orientation Claim 1; Page 44-46; 58pp; English.

An ElO chick brain cDNA library was screened with probes based on netrin-1 (p78) or netrin-2 (p75) sequences to isolate chick p78 and p75 partial cDNA clones. Full-length clones (given in Q92366-67, respectively) were subsequently obtd. by 3'RACE. cDNA is expressed e.g. in COS or insect cells for recombinant p78 and p75 prodn., used to breed transgenic animals, or for gene therapy
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285..453
/label = Domain V
/note = "domain V includes EGF-like repeats"
454..605
/note = "C-terminal region"
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  transgenic animal;
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46;
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Pred. No. 3.95e-02;
34; Mismatches 43
                                                                                                                                                                             ;ULT 10
R74186 standard; Protein; 605 AA.
R74186;
24-DEC-1995 (first entry)
Chick p78.
Neural axon out-growth modulator; epidermal netrin-1; p78; neurodegenerative disease; tr gene therapy.
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  Mismatches
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26..284
/label= Domain-VI
/note= "domain VI
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-NOV-1994; U12913.
-NOV-1993; US-152019.
EGC ) UNIV CALIFORNIA.
YCO ) UNIV COLUMBIA NEW YORK.
28;
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essed e.g. in cound
dn., used to breed to
e 605 AA;
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Best Local Similarity 26.1%;
Matches 31; Conservative
Conservative
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'label-
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50
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Dodd J, Jessell
Tessler-Lavigne M;
WPI; 95-194086/25.
"-PSDB; 092366.
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12-NOV-1
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(UYCO )
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Human netrin-1 protein and related nucleic acids - useful in modulating neuron growth and screening for compounds for diagnosis or treatment of diseases associated with undesirable growth or treatment of diseases associated with undesirable growth or treatment of diseases associated with undesirable growth or this protein comprises human netrin-1 (see W35946), a protein which is involved in neural axon guidance, and which is especially useful in modulating neural axon outgrowth. Its amino acid sequence was deduced from a cDNA clone (see T97129) isolated from a sequence with netrin (claimed).

Isolated netrin-1 can also be used to screen chemical libraries for candidate drugs suitable for diagnosis or treatment of diseases associated with undesirable neural cell growth, by comparing binding to a netrin binding target with and without the presence of a prospective agent. Agents that modulate the interaction may be useful as pharmaceutical lead compounds (claimed).

Sequence 604 AA;
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                                                                                 morphology;
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Pred. No. 7.10e-02;
30; Mismatches 49;
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therapy; drug s
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296..297
/note= "unidentified
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In-1; p78; neurodegenerative
therapy.
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ng Y;
                    604
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WO9740064-A1.
30-OCT-1997.
19-APR-1997; U06452.
19-APR-1996; US-635137.
(EXEL-) EXELIXIS PHARM INC.
(REGC.) UNIV CALIFORNIA.
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larity 24.8%;
Conservative
                                                                                     neuron; growth; sease; diagnosis;
                                                     entry)
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                 Protein;
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/note= "..
311
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393..39
/note=
487
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29; Conser
                   standard;
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W35946 standarc
W35946;
11-MAY-1998 (1
Human netrin-1
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R74188;
24-DEC-1995
Mouse p78
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This protein sequence comprises the human RECK protein (reversion-inducing cysteine rich protein with Kazal motif), which is capable of transforming malignant cancer cells with an activated ras gene into normal cells (reversion activity). Its amino acid sequence was deduced from a CDNA clone (see T90508) obtained from human fibroblast MRC-5 (ATCC CCL 171) cells. A claimed method for treatment of cancer comprises contacting the cancer cells with a RECK polypeptide. RECK may also be expressed using gene therapy methods for in vivo treatment of cancer.

Sequence 732 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        reversion
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                                                                                                                          netrin 1 or netrin 2 - comprise peptide(s) capable of selectives netrin 1 or netrin 2 - comprise peptide(s) capable of selectives increasing spinal axon out-growth or directing axon orientation claim 1; Page 51-52; 58pp; English.

Chick p75 and p78 sequences (given in R74186-87, respectively) were used to identify conserved amino acid regions, which were then used to design degenerate primers for the amplification of a fragment of the mouse p78 cDNA (092368). This cDNA can be expressed in host cells for recombinant p78 prodn, or used to breed transgenic animals, or for gene therapy.
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RECK cancer-inhibiting protein.
reversion-inducing cysteine rich protein with Kazal
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Pred. No. 1.50e+00
25; Mismatches 4
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/label - Kazal_doma
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WO9513367-A1.
18-MAY-1995.
08-NOV-1994; U12913.
12-NOV-1993; US-152019.
(REGC ) UNIV CALIFORNIA.
(UYCO ) UNIV COLUMBIA NEW YORK.
Dodd J, Jessell T, Kennedy T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Takahashi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     therapy;
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Local Similarity 23.5%;
les 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9724439-A1.
10-JUL-1997.
24-DEC-1996; U20812.
27-DEC-1995; JP-340469.
(KITA/) KITAYAMA H.
(NODA/) NODA M.
(TAKA/) TAKAHASHI C.
(SANY) SANKYO CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene
                                                                                 Dodd J, Jessell T,
Tessier-Lavigne M;
WPI; 95-194086/25.
N-PSDB; Q92368.
Neural axon out-gro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kitayama H, Noda N
WPI; 97-363675/33.
N-PSDB; T90508.
RECK gene and corre
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Claim 7; Page 4
This protein se
inducing cystei
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W26642 stand
W26642;
11-FEB-1998
Human RECY
RFCY
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Best Local
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Length

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100;

Score

Match

Query

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Helicobacter pylori nucleic acid sequences and encoded
To polypeptide(s) - useful in vaccines to treat or prevent H. pylori
To propertide(s) - useful in vaccines to treat or prevent H. pylori
To claim 14; Page 587-589; 1145pp; English.
This sequence is a H. pylori protein of unspecified function.
The protein may be used in a vaccine to prevent or treat H. pylori
To finection or to identify H. pylori polypeptide binding compounds,
To seful as potential H. pylori life cycle activators or inhibitors. The
To complemental H. pylori life cycle activators or inhibitors. The
The protein or to identify H. pylori life cycle activators or inhibitors. The
To box and probes derived from it may be used for the identification of
The pylori in a sample and the diagnosis of H. pylori infection. Nucleic
The pylori can be used in immunoassays to evaluate the abundance
against the protein can be used in immunoassays to evaluate the abundance
The pylori (ATCC 55679) was determined from overlapping contigs generated
To ORF of at least 180 nucleotides, and the predicted coding regions
To off or ORF of at least 180 nucleotides, and the predicted from various ORF
To were analysed for significant homology to other known or exported
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          n; envelope;
e; activator;
diagnosis.
                                                                            membrane proteins. Having identified and determined the sequences interest, particular regions can be isolated from H. pylori by PCI amplification for recombinant polypeptide production, e.g. in E.
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                              Indels
                                                                                                                                                                                                                                                                                                                               H. pylori ORF 09ap11406orf2 protein.
Cytoplasmic; vaccine; prevention; treatment; infection; identification; binding compound; bacteria; life cycle; inhibitor; duodenal ulcer disease; chronic gastritis; disease; chronic gastri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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No. 3.78e+00;
Mismatches 36;
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l. No. 4.53e+00;
Mismatches 19;
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Pred. No.
16; Misma
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larity 31.5%;
Conservative
 58;
 Similarity 30.5% 25; Conservative
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-1996; US-625811.
-1996; US-758731.
-1996; US-736905.
-1996; US-738859.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-OCT-1997. U05223. 27-MAR-1997; U05223. 06-DEC-1996; US-7613. 29-MAR-1996; US-7587. 25-OCT-1996; US-7388.
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Alm RA, Smith D;
WPI; 97-503122/46.
N-PSDB; V24777.
Helicobacter pylori
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les 17; Conse
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08-JUL-1994
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KW Enzyme; cyclosporin; synthetase-like activity; Tolypocladium niveum; T. inflatum GAMS: blosynthesis; vector; cyclosporin synthetase.

Tolypocladium niveum.

Ep-578616-A.

12-7AN-1994.

PD 12-7AN-1994.

PD 12-7AN-1994.

PR 09-UUL-1992; AT-001437.

PR 09-UUL-1992; AT-001437.

PR 09-UUL-1993; AT-000437.

PR 09-MAY-1993; CH-001376.

PR 09-MAY-1994; PR 09-MAY-1994.

PR 09-MAY-1994.

PR 09-MAY-1994; PR 09-MAY-1994.

PR 09-MAY-1994; PR 09-MAY-1994.

PR 09-MAY-1994; PR 09-MAY-1994.

PR 09-MAY-1994; PR 09-MAY-1
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lrgtkisdhiaianipnsktiverticesvydlgg-dakdsndrvswlsaa-rsnavkva 3876 231 Gaps ω .. Length 15281 Indels re 97; DB 9; Lend. No. 6.52e+00; Mismatches 35; 3906 259 Score 97; Pred. No. 23; Misma Query Match Best Local Similarity 26.7%; Matches 24; Conservative 3819 3877 176 232 g 8 ò ò

Search completed: Thu Oct 22 16:01:16 1998 Job time : 70 secs.